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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-671-074-41

Query Match      80.0%; Score 16; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGGCAAC 16
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Db 5 GCTTTGGTTGGGCAAC 20

RESULT 24
US-10-671-074-119/c
; Sequence 119, Application US/10671074
; Publication No. US20040097459A1
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Veniant-Ellison, Murielle
; APPLICANT: Lindberg, Richard A.
; APPLICANT: Shutter, John R.
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION
; FILE REFERENCE: AMGN0001-101
; CURRENT APPLICATION NUMBER: US/10/671,074
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-671-074-119

Query Match      80.0%; Score 16; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGGCAAC 16
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Db 16 GCTTTGGTTGGGCAAC 1

RESULT 25
US-09-764-891-7739
; Sequence 7739, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: FC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7739
; LENGTH: 4106
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7739

Query Match      80.0%; Score 16; DB 3; Length 4106;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGTTGGGCAACACA 19
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Db 1936 TTGGTTGGGCAACACA 1951
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RESULT 26
US-10-719-956-641503/c
; Sequence 641503, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 641503
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-641503

Query Match      75.0%; Score 15; DB 7; Length 25;
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Db 17 TTGGTTGGGCAACAC 3

RESULT 27
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; Sequence 643422, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 643422
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-643422

Query Match      75.0%; Score 15; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 GCTTGGGCAACACAT 16 51010172 751

RESULT 28
US-10-424-599-107214/c
; Sequence 107214, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2006, 16:00:58 ; Search time 85 Seconds  
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418.250 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20

Sequence: 1 gcttgggttggaacacat 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2605320

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	15	75.0	1342	US-08-976-259-66
5	15	75.0	1342	US-09-956-004-66
6	15	75.0	1701	US-09-543-681A-3630
7	15	75.0	2181	US-09-328-352-3989
8	15	75.0	3593	US-09-644-934-10
9	15	75.0	5205	US-09-724-126A-18
10	15	75.0	6308	US-09-724-126A-1
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12	15	75.0	1830121	US-09-557-884-1
13	15	75.0	1830121	US-09-643-990A-1
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15	15	75.0	349	US-09-513-999C-26749
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17	14	70.0	440	US-09-188-930-77
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21	14	70.0	601	US-09-949-016-158206
22	14	70.0	601	US-09-949-016-158206
23	14	70.0	707	US-09-442-143A-7
24	14	70.0	707	US-09-902-563-7

25	14	70.0	1194	US-09-583-110-2269	Sequence 2269, Ap
26	14	70.0	1194	US-09-107-433-294	Sequence 294, Ap
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c 29	14	70.0	1279	US-09-765-271-47	Sequence 47, Appl
c 30	14	70.0	1279	US-09-765-272A-47	Sequence 47, Appl
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c 33	14	70.0	1308	US-09-107-433-1653	Sequence 1279, Ap
c 34	14	70.0	1449	US-09-917-254-22	Sequence 1653, Ap
c 35	14	70.0	2184	US-09-949-016-4402	Sequence 22, Appl
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c 37	14	70.0	2743	US-08-818-823-3	Sequence 3, Appl
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c 43	14	70.0	2751	US-09-049-691-45	Sequence 45, Appl
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c 46	14	70.0	2751	US-09-037-192-45	Sequence 45, Appl
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c 48	14	70.0	2935	US-09-949-016-823	Sequence 823, Appl
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c 50	14	70.0	4152	US-09-540-236-1660	Sequence 1660, Ap
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c 78	13	65.0	224	US-09-270-767-21915	Sequence 21915, A
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c 84	13	65.0	417	US-09-270-767-18425	Sequence 18425, A
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c 86	13	65.0	535	US-09-270-767-1931	Sequence 1931, Ap
c 87	13	65.0	535	US-09-270-767-17213	Sequence 17213, A
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C 101	13	65.0	601	3	US-09-949-016-153559	Sequence 133559,	174	13	65.0	39443	3	US-09-949-016-14327	Sequence 14327, A
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C 103	13	65.0	601	3	US-09-949-016-169480	Sequence 169480,	c 176	13	65.0	40124	3	US-09-949-002-775	Sequence 775, App
C 104	13	65.0	601	3	US-09-949-016-169481	Sequence 169481,	c 177	13	65.0	42348	3	US-09-949-016-17157	Sequence 17157, A
C 105	13	65.0	601	3	US-09-949-016-174750	Sequence 174750,	c 178	13	65.0	44971	3	US-09-949-016-17049	Sequence 17049, A
C 106	13	65.0	601	3	US-09-949-016-174751	Sequence 174751,	179	13	65.0	51508	3	US-09-949-016-16681	Sequence 16681, A
C 107	13	65.0	603	3	US-09-540-236-1853	Sequence 1853,	180	13	65.0	54420	3	US-09-949-016-15422	Sequence 15422, A
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C 109	13	65.0	640	3	US-09-270-767-7378	Sequence 7378,	182	13	65.0	56904	3	US-09-949-016-15501	Sequence 15501, A
C 110	13	65.0	640	3	US-09-270-767-7378	Sequence 22660, A	183	13	65.0	58879	3	US-09-949-016-16052	Sequence 16052, A
C 111	13	65.0	831	3	US-09-252-991A-8588	Sequence 8588, Ap	c 184	13	65.0	67581	3	US-09-949-016-14768	Sequence 14768, A
C 112	13	65.0	918	2	US-08-743-637B-162	Sequence 162, App	c 185	13	65.0	67643	3	US-09-949-016-14760	Sequence 14760, A
C 113	13	65.0	918	3	US-08-526-840B-162	Sequence 162, App	c 186	13	65.0	69813	3	US-09-949-016-12455	Sequence 12455, A
C 114	13	65.0	963	3	US-09-252-991A-7371	Sequence 7371, Ap	c 187	13	65.0	69813	3	US-09-949-016-13905	Sequence 13905, A
C 115	13	65.0	979	3	US-09-270-767-13232	Sequence 13232, A	c 188	13	65.0	69813	3	US-09-949-016-13906	Sequence 13906, A
C 116	13	65.0	1041	2	US-08-580-545B-5	Sequence 5, Appli	c 189	13	65.0	69833	3	US-09-949-016-12861	Sequence 12861, A
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C 118	13	65.0	1050	3	US-09-252-991A-7130	Sequence 7130, Ap	c 191	13	65.0	80269	3	US-09-949-016-15681	Sequence 15681, A
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C 130	13	65.0	1475	3	US-09-419-362-30	Sequence 30, Appl	c 203	13	65.0	152132	3	US-09-949-016-13845	Sequence 13845, A
C 131	13	65.0	1475	3	US-09-419-362-32	Sequence 32, Appl	c 204	13	65.0	152145	3	US-09-949-016-12371	Sequence 12371, A
C 132	13	65.0	1656	3	US-09-248-796A-3263	Sequence 3263, Ap	c 205	13	65.0	155617	3	US-09-949-016-16191	Sequence 16191, A
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C 135	13	65.0	1860	3	US-09-248-796A-1590	Sequence 1590, Ap	c 208	13	65.0	187580	3	US-09-949-016-13266	Sequence 13266, A
C 136	13	65.0	1995	3	US-09-771-161A-31	Sequence 31, Appl	c 209	13	65.0	221545	3	US-09-949-016-13875	Sequence 13875, A
C 137	13	65.0	2311	3	US-08-800-729-66	Sequence 66, Appl	c 210	13	65.0	227979	3	US-09-949-016-11842	Sequence 11842, A
C 138	13	65.0	2388	3	US-09-205-258-154	Sequence 154, App	c 211	13	65.0	229354	3	US-09-705-400-64	Sequence 64, Appl
C 139	13	65.0	2388	3	US-10-004-860-154	Sequence 154, App	c 212	13	65.0	237241	3	US-09-949-016-16101	Sequence 16101, A
C 140	13	65.0	2394	3	US-09-800-729-33	Sequence 33, Appl	c 213	13	65.0	247299	3	US-09-949-016-17590	Sequence 17590, A
C 141	13	65.0	2502	3	US-09-252-991A-8656	Sequence 8656, Ap	c 214	13	65.0	340380	3	US-09-949-016-14179	Sequence 14179, A
C 142	13	65.0	2631	3	US-09-487-558B-43	Sequence 43, Appl	c 215	13	65.0	818128	3	US-09-949-016-14546	Sequence 14546, A
C 143	13	65.0	2667	3	US-09-303-518D-877	Sequence 877, App	c 216	13	65.0	818128	3	US-09-949-016-14547	Sequence 14547, A
C 144	13	65.0	2769	3	US-09-303-518D-883	Sequence 883, App	c 217	13	65.0	818128	3	US-09-949-016-14548	Sequence 14548, A
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C 146	13	65.0	2800	3	US-09-265-315-35	Sequence 35, Appl	c 219	13	65.0	818128	3	US-09-949-016-14550	Sequence 14550, A
C 147	13	65.0	2800	3	US-09-265-315-35	Sequence 35, Appl	c 220	13	65.0	818128	3	US-09-949-016-14551	Sequence 14551, A
C 148	13	65.0	2800	3	US-09-266-417-35	Sequence 35, Appl	c 221	13	65.0	818128	3	US-09-949-016-14552	Sequence 14552, A
C 149	13	65.0	2800	3	US-09-528-709-35	Sequence 35, Appl	c 222	13	65.0	818128	3	US-09-949-016-14553	Sequence 14553, A
C 150	13	65.0	2800	3	US-09-527-745-35	Sequence 35, Appl	c 223	13	65.0	818128	3	US-09-949-016-14554	Sequence 14554, A
C 151	13	65.0	4234	3	US-09-976-594-513	Sequence 513, App	c 224	13	65.0	818128	3	US-09-949-016-14555	Sequence 14555, A
C 152	13	65.0	4826	3	US-08-956-171E-275	Sequence 275, App	c 225	13	65.0	818128	3	US-09-949-016-14556	Sequence 14556, A
C 153	13	65.0	4826	3	US-08-781-986A-275	Sequence 275, App	c 226	13	65.0	818128	3	US-09-949-016-14557	Sequence 14557, A
C 154	13	65.0	5162	3	US-09-298-367B-1	Sequence 1, Appli	c 227	13	65.0	818128	3	US-09-949-016-14558	Sequence 14558, A
C 155	13	65.0	5162	3	US-09-298-367B-4	Sequence 4, Appli	c 228	13	65.0	818128	3	US-09-949-016-14559	Sequence 14559, A
C 156	13	65.0	5262	3	US-09-298-367B-5	Sequence 5, Appli	c 229	13	65.0	818128	3	US-09-949-016-14560	Sequence 14560, A
C 157	13	65.0	6360	3	US-09-171-699-9	Sequence 9, Appli	c 230	13	65.0	818128	3	US-09-949-016-14561	Sequence 14561, A
C 158	13	65.0	6850	3	US-09-298-367B-2	Sequence 2, Appli	c 231	13	65.0	818128	3	US-09-949-016-14562	Sequence 14562, A
C 159	13	65.0	7159	3	US-08-956-171E-302	Sequence 302, App	c 232	13	65.0	818128	3	US-09-949-016-14564	Sequence 14564, A
C 160	13	65.0	8035	3	US-09-949-016-14727	Sequence 14727, App	c 233	13	65.0	818128	3	US-09-949-016-14565	Sequence 14565, A
C 161	13	65.0	8617	3	US-09-949-016-14663	Sequence 14663, A	c 234	13	65.0	818128	3	US-09-949-016-14566	Sequence 14566, A
C 162	13	65.0	8617	3	US-09-949-016-14286	Sequence 14286, A	c 235	13	65.0	818128	3	US-09-949-016-14567	Sequence 14567, A
C 163	13	65.0	8618	3	US-09-949-016-14286	Sequence 14286, A	c 236	13	65.0	818128	3	US-09-482-180A-9	Sequence 9, Appli
C 164	13	65.0	14012	3	US-09-949-016-14625	Sequence 14625, A	c 237	12	60.0	36	3	US-09-569-601A-2	Sequence 2, Appli
C 165	13	65.0	15695	3	US-09-949-016-15644	Sequence 15644, A	c 238	12	60.0	36	3	US-09-569-601A-18	Sequence 18, Appli
C 166	13	65.0	23321	3	US-09-949-016-11936	Sequence 11936, A	c 239	12	60.0	133	3	US-09-513-999C-9885	Sequence 9885, Ap
C 167	13	65.0	23325	3	US-09-949-016-16622	Sequence 16622, A	c 240	12	60.0	136	3	US-09-471-276-704	Sequence 704, App
C 168	13	65.0	32099	3	US-09-949-016-16562	Sequence 16562, A	c 241	12	60.0	202	3	US-09-513-999C-23748	Sequence 23748, A
C 169	13	65.0	36855	3	US-09-949-016-17095	Sequence 17095, A	c 242	12	60.0	212	3	US-09-513-999C-18559	Sequence 18559, A
C 170	13	65.0	37613	3	US-09-949-016-12669	Sequence 12669, A	c 243	12	60.0	227	3	US-09-754-066-19	Sequence 19, Appli



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245	12	60.0	245	3	US-09-513-999C-10946	Sequence 10946, A	318	12	60.0	601	3	US-09-949-016-57074	Sequence 57074, A
246	12	60.0	247	3	US-09-513-999C-24147	Sequence 24147, A	319	12	60.0	601	3	US-09-949-016-57075	Sequence 57075, A
247	12	60.0	253	3	US-09-513-999C-25936	Sequence 25936, A	320	12	60.0	601	3	US-09-949-016-59627	Sequence 59627, A
248	12	60.0	266	3	US-09-313-294A-3633	Sequence 3633, App	c 321	12	60.0	601	3	US-09-949-016-60171	Sequence 60171, A
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251	12	60.0	336	3	US-09-513-999C-9569	Sequence 9569, App	324	12	60.0	601	3	US-09-949-016-62540	Sequence 62540, A
252	12	60.0	343	3	US-09-513-559-3747	Sequence 3747, App	325	12	60.0	601	3	US-09-949-016-62541	Sequence 62541, A
253	12	60.0	359	3	US-09-270-767-2723	Sequence 2723, App	326	12	60.0	601	3	US-09-949-016-62542	Sequence 62542, A
254	12	60.0	359	3	US-09-270-767-18005	Sequence 18005, A	327	12	60.0	601	3	US-09-949-016-62543	Sequence 62543, A
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256	12	60.0	365	3	US-09-513-999C-33710	Sequence 33710, A	329	12	60.0	601	3	US-09-949-016-63236	Sequence 63236, A
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258	12	60.0	390	3	US-09-711-164-248	Sequence 248, App	331	12	60.0	601	3	US-09-949-016-68607	Sequence 68607, A
259	12	60.0	393	3	US-09-489-039A-3764	Sequence 3764, App	332	12	60.0	601	3	US-09-949-016-69640	Sequence 69640, A
260	12	60.0	399	3	US-09-270-767-1659	Sequence 1659, App	c 333	12	60.0	601	3	US-09-949-016-69812	Sequence 69812, A
261	12	60.0	399	3	US-09-270-767-16941	Sequence 16941, A	c 334	12	60.0	601	3	US-09-949-016-69812	Sequence 69812, A
262	12	60.0	423	3	US-09-328-353-3580	Sequence 3580, App	c 335	12	60.0	601	3	US-09-949-016-76583	Sequence 76583, A
263	12	60.0	428	3	US-09-621-976-17842	Sequence 17842, A	c 336	12	60.0	601	3	US-09-949-016-78030	Sequence 78030, A
264	12	60.0	462	3	US-09-621-976-3261	Sequence 3261, App	c 337	12	60.0	601	3	US-09-949-016-80199	Sequence 80199, A
265	12	60.0	467	3	US-09-270-767-2240	Sequence 2240, A	338	12	60.0	601	3	US-09-949-016-80726	Sequence 80726, A
266	12	60.0	467	3	US-09-270-767-17822	Sequence 17822, A	339	12	60.0	601	3	US-09-949-016-80728	Sequence 80728, A
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268	12	60.0	471	2	US-09-197-816-1	Sequence 1, Appl	c 341	12	60.0	601	3	US-09-949-016-87362	Sequence 87362, A
269	12	60.0	486	3	US-09-252-991A-11364	Sequence 11364, A	c 342	12	60.0	601	3	US-09-949-016-91374	Sequence 91374, A
270	12	60.0	487	3	US-09-621-976-10207	Sequence 10207, A	c 343	12	60.0	601	3	US-09-949-016-92943	Sequence 92943, A
271	12	60.0	491	3	US-09-621-976-17740	Sequence 17740, A	c 344	12	60.0	601	3	US-09-949-016-107318	Sequence 107318, A
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273	12	60.0	505	3	US-09-270-767-21041	Sequence 21041, A	c 346	12	60.0	601	3	US-09-949-016-107423	Sequence 107423, A
274	12	60.0	505	3	US-09-270-767-6920	Sequence 6920, App	c 347	12	60.0	601	3	US-09-949-016-107431	Sequence 107431, A
275	12	60.0	508	3	US-09-270-767-22202	Sequence 22202, A	c 348	12	60.0	601	3	US-09-949-016-107432	Sequence 107432, A
276	12	60.0	508	3	US-09-058-389A-21	Sequence 21, Appl	349	12	60.0	601	3	US-09-949-016-108568	Sequence 108568, A
277	12	60.0	508	3	US-09-611-781-21	Sequence 21, Appl	350	12	60.0	601	3	US-09-949-016-108569	Sequence 108569, A
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279	12	60.0	509	3	US-09-270-767-24096	Sequence 24096, A	c 352	12	60.0	601	3	US-09-949-016-119478	Sequence 119478, A
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281	12	60.0	534	3	US-09-621-976-17102	Sequence 17102, A	c 354	12	60.0	601	3	US-09-949-016-127615	Sequence 127615, A
282	12	60.0	538	3	US-09-621-976-584	Sequence 584, App	c 355	12	60.0	601	3	US-09-949-016-127615	Sequence 127615, A
283	12	60.0	549	3	US-09-533-559-1306	Sequence 1306, App	c 356	12	60.0	601	3	US-09-949-016-127949	Sequence 127949, A
284	12	60.0	577	3	US-09-270-767-7037	Sequence 7037, App	c 357	12	60.0	601	3	US-09-949-016-127951	Sequence 127951, A
285	12	60.0	579	3	US-09-270-767-22319	Sequence 22319, A	c 358	12	60.0	601	3	US-09-949-016-127952	Sequence 127952, A
286	12	60.0	579	3	US-08-953-171-3	Sequence 33, Appl	c 359	12	60.0	601	3	US-09-949-016-133403	Sequence 133403, A
287	12	60.0	579	3	US-09-540-236-1408	Sequence 1408, App	c 360	12	60.0	601	3	US-09-949-016-137820	Sequence 137820, A
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289	12	60.0	595	2	US-08-285-641-5	Sequence 5, Appl	c 362	12	60.0	601	3	US-09-949-016-143169	Sequence 143169, A
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311	12	60.0	601	3	US-09-949-016-52562	Sequence 52562, A	c 384	12	60.0	601	3	US-09-949-016-180528	Sequence 180528, A
312	12	60.0	601	3	US-09-949-016-52563	Sequence 52563, A	c 385	12	60.0	601	3	US-09-949-016-180731	Sequence 180731, A
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C 391	12	60.0	601	3	US-09-949-016-197366	Sequence 197366,	464	12	60.0	1351	3	US-09-491-795-3	Sequence 3, Appli
C 392	12	60.0	601	3	US-09-949-016-197484	Sequence 197484,	465	12	60.0	1398	3	US-09-328-352-3200	Sequence 3200, Ap
C 393	12	60.0	601	3	US-09-949-016-199185	Sequence 199185,	466	12	60.0	1413	3	US-09-543-681A-3221	Sequence 3221, Ap
C 394	12	60.0	601	3	US-09-949-016-199906	Sequence 199906,	c 467	12	60.0	1419	3	US-09-540-236-1840	Sequence 1840, Ap
C 395	12	60.0	601	3	US-09-949-016-200360	Sequence 200360,	c 468	12	60.0	1420	3	US-09-482-180A-1	Sequence 1, Appli
C 396	12	60.0	601	3	US-09-949-016-200361	Sequence 200361,	c 469	12	60.0	1460	3	US-09-573-080A-364	Sequence 364, App
C 397	12	60.0	601	3	US-09-949-016-202637	Sequence 202637,	c 470	12	60.0	1605	3	US-09-252-991A-15515	Sequence 15515, A
C 398	12	60.0	601	3	US-09-949-002-2264	Sequence 2264, Ap	471	12	60.0	1701	2	US-08-484-993B-40	Sequence 40, Appl
C 399	12	60.0	601	3	US-09-949-002-2265	Sequence 2265, Ap	472	12	60.0	1701	2	US-08-484-158B-40	Sequence 40, Appl
C 400	12	60.0	601	3	US-09-949-002-2266	Sequence 2266, Ap	473	12	60.0	1701	2	US-08-484-596A-40	Sequence 40, Appl
C 401	12	60.0	601	3	US-09-949-002-8414	Sequence 8414, Ap	474	12	60.0	1701	2	US-08-480-150A-40	Sequence 40, Appl
C 402	12	60.0	601	3	US-09-949-002-8415	Sequence 8415, Ap	475	12	60.0	1701	2	US-08-458-731-40	Sequence 40, Appl
C 403	12	60.0	601	3	US-09-949-002-8416	Sequence 8416, Ap	476	12	60.0	1701	3	US-08-149-223A-40	Sequence 40, Appl
C 404	12	60.0	601	3	US-09-949-002-9535	Sequence 9535, Ap	c 477	12	60.0	1704	3	US-09-711-164-203	Sequence 203, App
C 405	12	60.0	601	3	US-09-949-002-9536	Sequence 9536, Ap	c 478	12	60.0	1719	3	US-09-248-796A-4662	Sequence 4662, Ap
C 406	12	60.0	601	3	US-08-949-002-9537	Sequence 9537, Ap	c 479	12	60.0	1759	3	US-10-104-047-1283	Sequence 1283, Ap
C 407	12	60.0	603	2	US-08-799-464A-21	Sequence 21, Appl	c 480	12	60.0	1788	3	US-09-404-296B-7	Sequence 7, Appli
C 408	12	60.0	603	6	PCT-US95-09927-21	Sequence 21, Appl	c 481	12	60.0	1801	2	US-09-130-114-3	Sequence 3, Appli
C 409	12	60.0	606	2	US-08-131-625B-12	Sequence 12, Appl	c 482	12	60.0	1845	3	US-08-476-102A-7	Sequence 7, Appli
C 410	12	60.0	606	3	US-08-855-531D-11	Sequence 11, Appl	483	12	60.0	1863	3	US-09-902-540-4947	Sequence 4947, Ap
C 411	12	60.0	606	3	US-08-855-526B-11	Sequence 11, Appl	484	12	60.0	1878	3	US-09-489-039A-2608	Sequence 2608, Ap
C 412	12	60.0	606	3	US-08-301-435-20	Sequence 20, Appl	c 485	12	60.0	1913	3	US-09-533-559-757	Sequence 757, App
C 413	12	60.0	606	6	PCT-US95-10904-20	Sequence 20, Appl	c 486	12	60.0	1936	3	US-09-249-585A-1	Sequence 1, Appli
C 414	12	60.0	612	3	US-09-280-116-218	Sequence 218, App	c 487	12	60.0	1937	3	US-09-050-863-1	Sequence 1, Appli
C 415	12	60.0	615	3	US-09-385-982-215	Sequence 215, App	c 488	12	60.0	1937	3	US-09-359-081-1	Sequence 1, Appli
C 416	12	60.0	618	3	US-09-270-767-8516	Sequence 8516, Ap	489	12	60.0	1944	3	US-08-392-806A-3	Sequence 3, Appli
C 417	12	60.0	618	3	US-09-270-767-23798	Sequence 23798, A	490	12	60.0	1944	3	US-09-257-490-3	Sequence 3, Appli
C 418	12	60.0	636	3	US-09-710-279-743	Sequence 743, App	491	12	60.0	1986	3	US-09-540-236-1823	Sequence 1823, Ap
C 419	12	60.0	636	3	US-09-533-559-6334	Sequence 6334, Ap	c 492	12	60.0	2036	3	US-10-104-047-1669	Sequence 1669, Ap
C 420	12	60.0	645	3	US-09-134-001C-538	Sequence 538, App	493	12	60.0	2145	3	US-09-712-363-3	Sequence 3, Appli
C 421	12	60.0	656	3	US-09-533-559-1100	Sequence 1100, App	c 494	12	60.0	2151	3	US-09-270-767-11481	Sequence 11481, A
C 422	12	60.0	662	3	US-09-669-751-49	Sequence 49, Appl	c 495	12	60.0	2156	2	US-08-321-356-1	Sequence 1, Appli
C 423	12	60.0	668	3	US-09-270-767-8513	Sequence 8513, Ap	c 496	12	60.0	2156	2	US-08-321-356-3	Sequence 3, Appli
C 424	12	60.0	668	3	US-09-270-767-23795	Sequence 23795, A	c 497	12	60.0	2172	3	US-09-543-681A-1285	Sequence 1285, Ap
C 425	12	60.0	672	3	US-09-280-116-217	Sequence 217, App	c 498	12	60.0	2175	3	US-10-101-464A-838	Sequence 838, App
C 426	12	60.0	672	3	US-08-778-717-6	Sequence 6, Appli	499	12	60.0	2241	3	US-09-710-279-651	Sequence 651, App
C 427	12	60.0	672	3	US-08-778-717-8	Sequence 8, Appli	500	12	60.0	2250	3	US-09-540-236-130	Sequence 130, App
C 428	12	60.0	690	3	US-08-778-717-18	Sequence 18, Appl	501	12	60.0	2256	3	US-08-969-415-1	Sequence 1, Appli
C 429	12	60.0	699	3	US-09-540-236-141	Sequence 141, App	502	12	60.0	2265	3	US-09-270-767-14284	Sequence 14284, A
C 430	12	60.0	702	3	US-09-248-796A-3522	Sequence 3522, Ap	c 503	12	60.0	2297	3	US-09-471-016-12	Sequence 12, Appl
C 431	12	60.0	726	3	US-09-540-236-432	Sequence 432, App	c 504	12	60.0	2304	3	US-10-104-047-294	Sequence 294, App
C 432	12	60.0	795	3	US-09-248-796A-1124	Sequence 1124, Ap	c 505	12	60.0	2312	3	US-10-104-047-488	Sequence 488, App
C 433	12	60.0	801	3	US-09-269-446D-38	Sequence 38, Appl	506	12	60.0	2322	3	US-09-328-352-4077	Sequence 4077, Ap
C 434	12	60.0	810	3	US-08-778-717-10	Sequence 10, Appl	507	12	60.0	2337	3	US-09-134-001C-1031	Sequence 1031, Ap
C 435	12	60.0	815	3	US-08-778-717-12	Sequence 12, Appl	508	12	60.0	2352	3	US-09-328-352-3064	Sequence 3064, Ap
C 436	12	60.0	819	3	US-09-328-352-3246	Sequence 3246, Ap	509	12	60.0	2381	3	US-10-104-047-1619	Sequence 1619, Ap
C 437	12	60.0	837	3	US-09-134-000C-201	Sequence 201, App	510	12	60.0	2396	3	US-09-058-389A-10	Sequence 10, Appl
C 438	12	60.0	866	2	US-08-484-993B-46	Sequence 46, Appl	511	12	60.0	2396	3	US-09-611-781-10	Sequence 10, Appl
C 439	12	60.0	866	2	US-08-484-158B-46	Sequence 46, Appl	c 512	12	60.0	2435	3	US-09-306-593-1	Sequence 1, Appli
C 440	12	60.0	866	2	US-08-484-596A-46	Sequence 46, Appl	513	12	60.0	2466	3	US-09-363-243-1	Sequence 1, Appli
C 441	12	60.0	866	2	US-08-480-150A-46	Sequence 46, Appl	514	12	60.0	2621	3	US-08-817-441-63	Sequence 63, Appl
C 442	12	60.0	866	3	US-08-458-731-46	Sequence 46, Appl	515	12	60.0	2649	3	US-10-104-047-847	Sequence 847, App
C 443	12	60.0	866	3	US-08-149-223A-46	Sequence 46, Appl	516	12	60.0	2656	3	US-09-949-016-4867	Sequence 4867, Ap
C 444	12	60.0	870	3	US-09-710-279-63	Sequence 63, Appl	517	12	60.0	2682	3	US-09-614-221A-222	Sequence 222, App
C 445	12	60.0	989	3	US-09-671-317-283	Sequence 283, App	c 518	12	60.0	2742	3	US-09-328-352-2898	Sequence 2898, Ap
C 446	12	60.0	1020	3	US-09-477-135A-120	Sequence 120, App	c 519	12	60.0	2742	3	US-09-949-016-4295	Sequence 4295, Ap
C 447	12	60.0	1074	3	US-09-807-757C-5	Sequence 5, Appli	c 520	12	60.0	2743	2	US-08-317-707-1	Sequence 1, Appli
C 448	12	60.0	1083	3	US-09-602-777A-259	Sequence 259, App	521	12	60.0	2754	3	US-10-104-047-954	Sequence 954, App
C 449	12	60.0	1101	3	US-09-328-352-910	Sequence 910, App	c 522	12	60.0	2797	3	US-09-949-016-853	Sequence 853, Appl
C 450	12	60.0	1179	3	US-09-710-279-3305	Sequence 3305, Ap	c 523	12	60.0	2821	3	US-10-104-047-565	Sequence 565, App
C 451	12	60.0	1194	3	US-09-543-681A-1349	Sequence 1349, Ap	c 524	12	60.0	2887	3	US-09-949-016-3493	Sequence 3493, Ap
C 452	12	60.0	1197	3	US-09-134-001C-1516	Sequence 1516, Ap	c 525	12	60.0	2948	3	US-09-949-016-1106	Sequence 1106, Ap
C 453	12	60.0	1211	3	US-09-270-767-30424	Sequence 30424, A	c 526	12	60.0	2949	3	US-09-949-016-4761	Sequence 4761, Ap
C 454	12	60.0	1218	3	US-10-012-231A-5	Sequence 5, Appli	c 527	12	60.0	3032	3	US-09-710-279-3924	Sequence 3924, Ap
C 455	12	60.0	1218	3	US-10-015-389A-5	Sequence 5, Appli	528	12	60.0	3137	3	US-09-710-279-3842	Sequence 3842, Ap
C 456	12	60.0	1218	3	US-10-006-768A-5	Sequence 5, Appli	529	12	60.0	3141	2	US-08-658-665-66	Sequence 66, Appl
C 457	12	60.0	1218	3	US-10-015-671A-5	Sequence 5, Appli	530	12	60.0	3141	3	US-08-796-101-30	Sequence 30, Appl
C 458	12	60.0	1218	3	US-10-015-393A-5	Sequence 5, Appli	531	12	60.0	3141	3	US-09-085-273-66	Sequence 66, Appl
C 459	12	60.0	1218	3	US-10-011-833A-5	Sequence 5, Appli	532	12	60.0	3141	3	US-09-916-963-66	Sequence 66, Appl
C 460	12	60.0	1218	3	US-10-006-041A-5	Sequence 5, Appli	533	12	60.0	3370	3	US-09-710-279-4190	Sequence 4190, Ap
C 461	12	60.0	1218	3	US-10-012-064A-5	Sequence 5, Appli	534	12	60.0	3517	3	US-09-221-017B-281	Sequence 281, App
C 462	12	60.0	1227	3	US-09-252-991A-15322	Sequence 15322, A	c 535	12	60.0	3531	3	US-09-949-016-2301	Sequence 2301, Ap

C 536	12	60.0	3567	2	US-08-658-665-69	Sequence 69, Appl	C 609	12	60.0	9737	3	US-09-481-355-22	Sequence 22, Appl
C 537	12	60.0	3567	3	US-08-796-101-33	Sequence 33, Appl	C 610	12	60.0	9737	3	US-09-481-355-23	Sequence 23, Appl
C 538	12	60.0	3567	3	US-09-085-273-69	Sequence 69, Appl	C 611	12	60.0	9737	3	US-09-481-355-28	Sequence 28, Appl
C 539	12	60.0	3567	3	US-09-916-963-69	Sequence 69, Appl	C 612	12	60.0	9737	3	US-09-481-282-22	Sequence 22, Appl
C 540	12	60.0	3569	3	US-09-710-279-4443	Sequence 4443, Ap	C 613	12	60.0	9737	3	US-09-481-282-23	Sequence 23, Appl
C 541	12	60.0	3591	3	US-09-614-221A-336	Sequence 336, Appl	C 614	12	60.0	9737	3	US-09-481-282-28	Sequence 28, Appl
C 542	12	60.0	3592	3	US-09-775-398-84	Sequence 84, Appl	C 615	12	60.0	9737	3	US-09-455-659A-22	Sequence 22, Appl
C 543	12	60.0	3596	3	US-09-949-016-2135	Sequence 2135, Ap	C 616	12	60.0	9737	3	US-09-455-659A-23	Sequence 23, Appl
C 544	12	60.0	3716	3	US-09-999-833A-210	Sequence 210, App	C 617	12	60.0	9737	3	US-09-455-659A-28	Sequence 28, Appl
C 545	12	60.0	3716	3	US-10-020-445A-210	Sequence 210, App	C 618	12	60.0	9737	3	US-09-484-996-22	Sequence 22, Appl
C 546	12	60.0	3764	3	US-09-949-016-4511	Sequence 4511, Ap	C 619	12	60.0	9737	3	US-09-484-996-23	Sequence 23, Appl
C 547	12	60.0	3816	3	US-09-540-236-1820	Sequence 1820, Ap	C 620	12	60.0	9737	3	US-09-484-996-28	Sequence 28, Appl
C 548	12	60.0	3845	3	US-09-620-312D-554	Sequence 554, App	C 621	12	60.0	9737	3	US-09-479-123-22	Sequence 22, Appl
C 549	12	60.0	3871	3	US-09-949-016-631	Sequence 631, App	C 622	12	60.0	9737	3	US-09-479-123-23	Sequence 23, Appl
C 550	12	60.0	3941	3	US-09-408-865-2	Sequence 2, Appll	C 623	12	60.0	9737	3	US-09-479-123-28	Sequence 28, Appl
C 551	12	60.0	4010	3	US-09-710-279-3540	Sequence 3540, Ap	C 624	12	60.0	9737	3	US-09-484-317A-22	Sequence 22, Appl
C 552	12	60.0	4019	3	US-09-710-279-4210	Sequence 4210, Ap	C 625	12	60.0	9737	3	US-09-484-317A-23	Sequence 23, Appl
C 553	12	60.0	4032	2	US-08-107-748-3	Sequence 3, Appll	C 626	12	60.0	9737	3	US-09-484-317A-28	Sequence 28, Appl
C 554	12	60.0	4032	2	US-08-245-809-4	Sequence 4, Appll	C 627	12	60.0	9737	3	US-09-276-820A-22	Sequence 22, Appl
C 555	12	60.0	4032	6	PCT-US92-01385-3	Sequence 3, Appll	C 628	12	60.0	9737	3	US-09-276-820A-23	Sequence 23, Appl
C 556	12	60.0	4076	3	US-09-710-273-4287	Sequence 4287, Ap	C 629	12	60.0	9737	3	US-09-276-820A-28	Sequence 28, Appl
C 557	12	60.0	4076	2	US-08-658-665-67	Sequence 67, Appl	C 630	12	60.0	9837	3	US-09-221-017B-636	Sequence 636, App
C 558	12	60.0	4075	3	US-08-796-101-31	Sequence 31, Appl	C 631	12	60.0	9871	3	US-09-479-122-24	Sequence 24, Appl
C 559	12	60.0	4075	3	US-09-085-273-67	Sequence 67, Appl	C 632	12	60.0	9871	3	US-09-481-355-24	Sequence 24, Appl
C 560	12	60.0	4075	3	US-09-916-963-67	Sequence 67, Appl	C 633	12	60.0	9871	3	US-09-481-355-24	Sequence 24, Appl
C 561	12	60.0	4286	3	US-08-227-800A-2	Sequence 2, Appll	C 634	12	60.0	9871	3	US-09-455-659A-24	Sequence 24, Appl
C 562	12	60.0	4286	3	US-08-921-954-2	Sequence 4, Appll	C 635	12	60.0	9871	3	US-09-484-996-24	Sequence 24, Appl
C 563	12	60.0	4290	3	US-08-924-629C-4	Sequence 4, Appll	C 636	12	60.0	9871	3	US-09-484-996-24	Sequence 24, Appl
C 564	12	60.0	4297	3	US-09-710-279-4092	Sequence 4092, Ap	C 637	12	60.0	9871	3	US-09-479-123-24	Sequence 24, Appl
C 565	12	60.0	4459	3	US-09-363-243-2	Sequence 2, Appll	C 638	12	60.0	9871	3	US-09-484-317A-24	Sequence 24, Appl
C 566	12	60.0	4531	3	US-09-620-312D-893	Sequence 893, App	C 639	12	60.0	9871	3	US-09-276-820A-24	Sequence 24, Appl
C 567	12	60.0	4537	3	US-09-254-321-1	Sequence 1, Appll	C 640	12	60.0	10060	3	US-09-479-122-25	Sequence 25, Appl
C 568	12	60.0	4909	2	US-08-658-665-68	Sequence 68, Appl	C 641	12	60.0	10060	3	US-09-484-997-25	Sequence 25, Appl
C 569	12	60.0	4909	3	US-08-796-101-32	Sequence 32, Appl	C 642	12	60.0	10060	3	US-09-481-355-25	Sequence 25, Appl
C 570	12	60.0	4909	3	US-09-085-273-68	Sequence 68, Appl	C 643	12	60.0	10060	3	US-09-481-355-25	Sequence 25, Appl
C 571	12	60.0	4909	3	US-09-916-963-68	Sequence 68, Appl	C 644	12	60.0	10060	3	US-09-455-659A-25	Sequence 25, Appl
C 572	12	60.0	5111	3	US-09-004-838-118	Sequence 118, App	C 645	12	60.0	10060	3	US-09-484-996-25	Sequence 25, Appl
C 573	12	60.0	5443	3	US-09-079-415-5	Sequence 5, Appll	C 646	12	60.0	10060	3	US-09-479-123-25	Sequence 25, Appl
C 574	12	60.0	5443	3	US-08-750-458A-1	Sequence 1, Appll	C 647	12	60.0	10060	3	US-09-484-317A-25	Sequence 25, Appl
C 575	12	60.0	6360	3	US-09-171-699-9	Sequence 9, Appll	C 648	12	60.0	10060	3	US-09-276-820A-25	Sequence 25, Appl
C 576	12	60.0	6436	3	US-09-949-016-16408	Sequence 16408, A	C 649	12	60.0	10580	2	US-08-196-259-1	Sequence 1, Appll
C 577	12	60.0	6749	2	US-08-658-665-71	Sequence 71, Appl	C 650	12	60.0	10596	2	US-07-884-811-15	Sequence 15, Appl
C 578	12	60.0	6749	2	US-08-658-665-177	Sequence 177, App	C 651	12	60.0	10596	2	US-07-885-971-15	Sequence 15, Appl
C 579	12	60.0	6749	3	US-08-796-101-35	Sequence 35, Appl	C 652	12	60.0	10596	2	US-08-087-783A-15	Sequence 15, Appl
C 580	12	60.0	6749	3	US-08-796-101-38	Sequence 38, Appl	C 653	12	60.0	10596	2	US-08-194-088B-15	Sequence 15, Appl
C 581	12	60.0	6749	3	US-09-085-273-71	Sequence 71, Appl	C 654	12	60.0	10596	2	US-08-194-087-15	Sequence 15, Appl
C 582	12	60.0	6749	3	US-09-916-963-71	Sequence 71, Appl	C 655	12	60.0	10596	6	PCT-US93-04648-15	Sequence 15, Appl
C 583	12	60.0	6799	3	US-10-017-754-1883	Sequence 1883, Ap	C 656	12	60.0	11437	3	US-09-949-002-587	Sequence 587, App
C 584	12	60.0	7808	3	US-09-453-702B-247	Sequence 247, App	C 657	12	60.0	11563	3	US-09-902-540-1019	Sequence 1019, App
C 585	12	60.0	7808	3	US-10-114-170-247	Sequence 247, App	C 658	12	60.0	11589	3	US-09-949-002-826	Sequence 826, App
C 586	12	60.0	8374	3	US-09-949-016-11911	Sequence 11911, A	C 659	12	60.0	11616	2	US-08-196-259-2	Sequence 2, Appll
C 587	12	60.0	8501	3	US-09-298-367B-6	Sequence 6, Appll	C 660	12	60.0	12023	3	US-09-949-016-16253	Sequence 16253, A
C 588	12	60.0	8540	3	US-08-487-283A-4	Sequence 4, Appll	C 661	12	60.0	12270	3	US-09-949-016-16892	Sequence 16892, A
C 589	12	60.0	8540	6	PCT-US96-05611A-12	Sequence 12, Appl	C 662	12	60.0	12270	3	US-09-949-002-830	Sequence 830, App
C 590	12	60.0	8575	6	PCT-US92-08238-6	Sequence 6, Appll	C 663	12	60.0	12285	3	US-09-949-016-16609	Sequence 16609, A
C 591	12	60.0	8640	3	US-09-964-956-24	Sequence 24, Appl	C 664	12	60.0	12377	3	US-09-949-016-12921	Sequence 12921, A
C 592	12	60.0	8640	3	US-09-964-956-26	Sequence 26, Appl	C 665	12	60.0	12440	3	US-09-949-016-14109	Sequence 14109, A
C 593	12	60.0	8705	3	US-09-647-344A-14	Sequence 14, Appl	C 666	12	60.0	12440	3	US-09-949-016-14110	Sequence 14110, A
C 594	12	60.0	8735	3	US-09-573-080A-19	Sequence 19, Appl	C 667	12	60.0	12440	3	US-09-949-016-14899	Sequence 14899, A
C 595	12	60.0	8831	3	US-09-949-016-15504	Sequence 15504, A	C 668	12	60.0	12440	3	US-09-949-016-14900	Sequence 14900, A
C 596	12	60.0	8885	3	US-09-634-238-26	Sequence 26, Appl	C 669	12	60.0	12759	3	US-09-949-016-16299	Sequence 16299, A
C 597	12	60.0	8932	2	US-08-252-493C-8	Sequence 8, Appll	C 670	12	60.0	12759	3	US-09-949-016-16300	Sequence 16300, A
C 598	12	60.0	8932	2	US-09-276-197-8	Sequence 8, Appll	C 671	12	60.0	12759	3	US-09-949-016-16301	Sequence 16301, A
C 599	12	60.0	9132	3	US-09-949-016-13642	Sequence 13642, A	C 672	12	60.0	12759	3	US-09-949-016-16302	Sequence 16302, A
C 600	12	60.0	9132	3	US-09-949-016-13070	Sequence 13070, A	C 673	12	60.0	12759	3	US-09-949-016-16303	Sequence 16303, A
C 601	12	60.0	9600	3	US-08-910-647-1	Sequence 1, Appll	C 674	12	60.0	12759	3	US-09-949-016-16304	Sequence 16304, A
C 602	12	60.0	9600	3	US-09-620-925-1	Sequence 1, Appll	C 675	12	60.0	12759	3	US-09-949-016-16305	Sequence 16305, A
C 603	12	60.0	9737	3	US-09-479-122-22	Sequence 22, Appl	C 676	12	60.0	12768	3	US-09-949-016-14302	Sequence 14302, A
C 604	12	60.0	9737	3	US-09-479-122-23	Sequence 23, Appl	C 677	12	60.0	12768	3	US-09-949-016-14303	Sequence 14303, A
C 605	12	60.0	9737	3	US-09-479-122-28	Sequence 28, Appl	C 678	12	60.0	12768	3	US-09-949-016-14304	Sequence 14304, A
C 606	12	60.0	9737	3	US-09-484-997-22	Sequence 22, Appl	C 679	12	60.0	12768	3	US-09-949-016-14305	Sequence 14305, A
C 607	12	60.0	9737	3	US-09-484-997-23	Sequence 23, Appl	C 680	12	60.0	12768	3	US-09-949-016-14306	Sequence 14306, A
C 608	12	60.0	9737	3	US-09-484-997-28	Sequence 28, Appl	C 681	12	60.0	12768	3	US-09-949-016-14307	Sequence 14307, A

682	12	60.0	12768	3	US-09-949-016-14308	Sequence 14308, A	c 755	12	60.0	33720	3	US-09-949-016-11910	Sequence 11910, A
683	12	60.0	12768	3	US-09-949-016-14309	Sequence 14309, A	c 756	12	60.0	33721	3	US-09-949-016-15467	Sequence 15467, A
684	12	60.0	12768	3	US-09-949-016-14310	Sequence 14310, A	c 757	12	60.0	34001	3	US-09-596-002-18	Sequence 18, Appl
685	12	60.0	12768	3	US-09-949-016-14311	Sequence 14311, A	c 758	12	60.0	36103	3	US-09-949-016-16382	Sequence 16382, A
686	12	60.0	12768	3	US-09-949-016-14312	Sequence 14312, A	c 759	12	60.0	36731	3	US-09-949-016-13770	Sequence 13770, A
687	12	60.0	12768	3	US-09-949-016-14313	Sequence 14313, A	c 760	12	60.0	37288	3	US-09-949-016-14593	Sequence 14593, A
688	12	60.0	12768	3	US-09-949-016-14314	Sequence 14314, A	c 761	12	60.0	37288	3	US-09-949-016-14594	Sequence 14594, A
689	12	60.0	12768	3	US-09-949-016-14315	Sequence 14315, A	c 762	12	60.0	37288	3	US-09-949-016-15847	Sequence 15847, A
690	12	60.0	12768	3	US-09-949-016-14316	Sequence 14316, A	c 763	12	60.0	37792	3	US-09-949-016-12503	Sequence 12503, A
691	12	60.0	13953	3	US-09-738-884-3	Sequence 3, Appl	c 764	12	60.0	37795	3	US-09-949-016-14263	Sequence 14263, A
692	12	60.0	13953	3	US-10-096-961A-3	Sequence 3, Appl	c 765	12	60.0	38653	3	US-09-922-445-1	Sequence 1, Appl
693	12	60.0	14497	3	US-09-949-016-16088	Sequence 16088, A	c 766	12	60.0	38653	3	US-09-949-016-13788	Sequence 13788, A
694	12	60.0	15101	2	US-08-799-464A-14	Sequence 14, Appl	c 767	12	60.0	38855	3	US-09-973-278-930	Sequence 930, App
695	12	60.0	15101	6	PCT-US95-09927-14	Sequence 14, Appl	c 768	12	60.0	39176	3	US-09-949-016-17603	Sequence 17603, A
696	12	60.0	15108	2	US-08-157-005-1	Sequence 1, Appl	c 769	12	60.0	39318	3	US-09-949-016-13798	Sequence 13798, A
697	12	60.0	15108	3	US-08-747-863-1	Sequence 1, Appl	c 770	12	60.0	40085	3	US-08-311-731A-26	Sequence 26, Appl
698	12	60.0	15108	3	US-09-565-864-1	Sequence 1, Appl	c 771	12	60.0	40493	3	US-09-949-016-15453	Sequence 15453, A
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## ALIGNMENTS

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RESULT 1
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; Patent No. 6777182
; GENERAL INFORMATION:
; APPLICANT: Baban, Soheyl
; APPLICANT: Bernard, Monique
; APPLICANT: Cherry, Elana
; APPLICANT: Gosselin, Diane
; APPLICANT: Hugo, Patrice
; APPLICANT: Malette, Brigitte
; APPLICANT: Miron, Pierre
; APPLICANT: Prive, Charles
; APPLICANT: Shazand, Kamran
; TITLE OF INVENTION: ENDOMETRIOSIS-RELATED MARKERS AND USES THEREOF
; FILE REFERENCE: 5600.71
; CURRENT APPLICATION NUMBER: US/09/794,928A
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/225,745
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: US 60/185,063
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 254
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US-09-794-928A-12
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; Sequence 16598, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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US-09-949-016-16598

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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US-09-949-016-42568
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RESULT 4
US-08-976-259-66
; Sequence 66, Application US/08976259
; Patent No. 6316609
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Choi, Gil H.
```



APPLICANT: Welch, Rodney A.  
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli  
Patent No. 6316609  
NUMBER OF SEQUENCES: 142  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Ave, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
FILING DATE: Herewith  
APPLICATION NUMBER: US/08/976,259  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/031,626 AND US 60/061,953  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CEM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1342 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-976-259-66

Query Match 75.0%; Score 15; DB 3; Length 1342;  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5  
US-09-956-004-66  
Sequence 66, Application US/09956004  
Patent No. 6787643  
GENERAL INFORMATION:  
APPLICANT: Patrick J. Dillon et al.  
TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands  
FILE REFERENCE: PB324D1  
CURRENT APPLICATION NUMBER: US/09/956,004  
CURRENT FILING DATE: 2001-09-20  
PRIOR APPLICATION NUMBER: 08/976,259  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/061,953  
PRIOR FILING DATE: 1997-10-14  
PRIOR APPLICATION NUMBER: 60/031,626  
PRIOR FILING DATE: 1996-11-22  
NUMBER OF SEQ ID NOS: 142  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 66  
LENGTH: 1342  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1238)..(1238)  
OTHER INFORMATION: n equals a, t, g, or c  
US-09-956-004-66

Query Match 75.0%; Score 15; DB 3; Length 1342;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAA 15  
|||||  
Db 614 GCTTTGGTTGGCAA 628

RESULT 6  
US-09-543-681A-3630  
Sequence 3630, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 3630  
LENGTH: 1701  
TYPE: DNA  
ORGANISM: Proteus mirabilis  
US-09-543-681A-3630

Query Match 75.0%; Score 15; DB 3; Length 1701;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGGTTGGCAACAC 18  
|||||  
Db 1271 TTGGTTGGCAACAC 1285

RESULT 7  
US-09-328-352-3989  
Sequence 3989, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 3989  
LENGTH: 2181  
TYPE: DNA  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-3989

Query Match 75.0%; Score 15; DB 3; Length 2181;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAA 15  
|||||  
Db 884 GCTTTGGTTGGCAA 898

RESULT 8  
US-09-645-069-22  
Sequence 22, Application US/09645069  
Patent No. 6808710  
GENERAL INFORMATION:  
APPLICANT: Clive Wood  
APPLICANT: Gordon Freeman

; TITLE OF INVENTION: PD-1, A Receptor For B7-4, and Uses Therefor  
; FILE REFERENCE: GNN-004B  
; CURRENT APPLICATION NUMBER: US/09/645,069  
; CURRENT FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: 60/150,390  
; PRIOR FILING DATE: 1999-8-23  
; PRIOR APPLICATION NUMBER: 60/164,897  
; PRIOR FILING DATE: 1999-11-10  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 3593  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (17)..(889)  
US-09-645-069-22

Query Match 75.0%; Score 15; DB 3; Length 3593;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTGGGCAACACAT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3406 GGTGGGCAACACAT 3420

RESULT 9  
US-09-644-934-10  
; Sequence 10, Application US/09644934  
; Patent No. 6936704  
; GENERAL INFORMATION:  
; APPLICANT: Gordon Freeman  
; APPLICANT: Vassiliki Boussiottis  
; APPLICANT: Tatyana Chernova  
; APPLICANT: Nelly Malenkovich  
; TITLE OF INVENTION: NOVEL B7-4 FAMILY MOLECULES AND USES THEREFOR  
; FILE REFERENCE: GNN-004A  
; CURRENT APPLICATION NUMBER: US/09/644,934  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/150,390  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 3593  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (17)..(889)  
US-09-644-934-10

Query Match 75.0%; Score 15; DB 3; Length 3593;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTGGGCAACACAT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3406 GGTGGGCAACACAT 3420

RESULT 10  
US-09-724-126A-18  
; Sequence 18, Application US/09724126A  
; Patent No. 6706505  
; GENERAL INFORMATION:  
; APPLICANT: Han, Hui-Quan  
; APPLICANT: Kwak, Keith  
; TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase Family  
; FILE REFERENCE: 01017/35966A  
; CURRENT APPLICATION NUMBER: US/09/724,126A

; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 60/187,211  
; PRIOR FILING DATE: 1999-03-01  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 18  
; LENGTH: 5205  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (662)  
; OTHER INFORMATION: n = A or T or G or C  
; NAME/KEY: misc feature  
; LOCATION: (668)  
; OTHER INFORMATION: n = A or T or G or C  
US-09-724-126A-18

Query Match 75.0%; Score 15; DB 3; Length 5205;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTGGGCAACACAT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1518 GGTGGGCAACACAT 1532

RESULT 11  
US-09-724-126A-1  
; Sequence 1, Application US/09724126A  
; Patent No. 6706505  
; GENERAL INFORMATION:  
; APPLICANT: Han, Hui-Quan  
; APPLICANT: Kwak, Keith  
; TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase Family  
; FILE REFERENCE: 01017/35966A  
; CURRENT APPLICATION NUMBER: US/09/724,126A  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 60/187,211  
; PRIOR FILING DATE: 1999-03-01  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 6308  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (696)..(5942)  
US-09-724-126A-1

Query Match 75.0%; Score 15; DB 3; Length 6308;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTGGGCAACACAT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2258 GGTGGGCAACACAT 2272

RESULT 12  
US-09-949-016-12968/c  
; Sequence 12968, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20



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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12968
; LENGTH: 222452
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-12968

Query Match          75.0%; Score 15; DB 3; Length 222452;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGGTTGGCAACACA 19
Db 179856 TGGTTGGCAACACA 179842

RESULT 13
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match          75.0%; Score 15; DB 3; Length 1830121;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAA 15
Db 1130570 GCTTTGGTTGGGCAA 1130584

RESULT 14
US-09-643-990A-1
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
; Owen White
; Hamilton O. Smith
; J. Craig Venter
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville,
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,990A
; FILING DATE: 23-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,429
; FILING DATE: 1995-06-07
; APPLICATION NUMBER: 08/426,787
; FILING DATE: 1995-04-21
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB186P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5790
; TELEFAX: 310-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match          75.0%; Score 15; DB 3; Length 1830121;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAA 15
Db 1130570 GCTTTGGTTGGGCAA 1130584

RESULT 15
US-10-158-865-1
; Sequence 1, Application US/10158865
; Patent No. 6846651
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Frag
; Patent No. 6846651
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P2C1D1
; CURRENT APPLICATION NUMBER: US/10/158,865
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; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US 09/557,884  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 08/476,102  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: US 08/426,787  
; PRIOR FILING DATE: 1995-04-21  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1830121  
; TYPE: DNA  
; ORGANISM: Haemophilus influenzae  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4747)..(4747)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (9921)..(9921)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (10150)..(10150)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (29298)..(29298)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (36543)..(36543)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (36551)..(36551)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (36636)..(36636)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (40808)..(40810)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (44416)..(44416)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (44905)..(44905)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (44975)..(44975)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (45593)..(45593)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (45732)..(45732)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (47036)..(47036)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (51334)..(51334)  
; OTHER INFORMATION: n equals a,t,c, or g

; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (51602)..(51602)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (51786)..(51786)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (51805)..(51805)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (55369)..(55369)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (65309)..(65309)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (65313)..(65313)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (80024)..(80024)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (100091)..(100091)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (102696)..(102696)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (105121)..(105121)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (107248)..(107248)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (117136)..(117136)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (119750)..(119750)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (119924)..(119924)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (120038)..(120038)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (121344)..(121344)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (122167)..(122167)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (122336)..(122336)  
; OTHER INFORMATION: n equals a,t,c, or g  
; FEATURE:



```
RESULT 18
US-09-188-930-77
; Sequence 77, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188.930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 440
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (9)...(9)
US-09-188-930-77

Query Match          70.0%; Score 14; DB 3; Length 440;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TTTGTTGGGCAAC 16
Db      401 TTGTTGGGCAAC 414

RESULT 19
US-09-949-016-27657/c
; Sequence 27657, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27657
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-27657

Query Match          70.0%; Score 14; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GGTGGGCAACACA 19
Db      284 GGTGGGCAACACA 271

RESULT 20
US-09-949-016-34062
; Sequence 34062, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34062
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-34062

Query Match          70.0%; Score 14; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 TGGTTGGGCAACAC 18
Db      413 TGGTTGGGCAACAC 426

RESULT 21
US-09-949-016-158206/c
; Sequence 158206, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 158206
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-158206

Query Match          70.0%; Score 14; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GGTGGGCAACACA 19
Db      284 GGTGGGCAACACA 271

RESULT 22
US-09-949-016-186133
; Sequence 186133, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186133
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-186133

Query Match          70.0%; Score 14; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAACAC 18
    |||||
Db 413 TGGTTGGGCAACAC 426

RESULT 23
US-09-442-143A-7
; Sequence 7, Application US/09442143A
; Patent No. 6403089
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09/442,143A
; CURRENT FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 707
; TYPE: DNA
; ORGANISM: Murine
; US-09-442-143A-7

Query Match          70.0%; Score 14; DB 3; Length 707;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTGGTTGGGCAAC 16
    |||||
Db 232 TTTGGTTGGGCAAC 245

RESULT 24
US-09-902-563-7
; Sequence 7, Application US/09902563
; Patent No. 6805863
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT APPLICATION NUMBER: US/09/902,563
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/442,143
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 7
; LENGTH: 707
; TYPE: DNA
; ORGANISM: Murine
; US-09-902-563-7

Query Match          70.0%; Score 14; DB 3; Length 707;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTGGTTGGGCAAC 16
    |||||
Db 232 TTTGGTTGGGCAAC 245

RESULT 25
US-09-583-110-2269
; Sequence 2269, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2269
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; US-09-583-110-2269

Query Match          70.0%; Score 14; DB 3; Length 1194;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTGGTTGGGCAAC 16
    |||||
Db 448 TTTGGTTGGGCAAC 461

RESULT 26
US-09-107-433-294
; Sequence 294, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 294:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1194 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...1194
; SEQUENCE DESCRIPTION: SEQ ID NO: 294:
US-09-107-433-294

Query Match 70.0%; Score 14; DB 3; Length 1194;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTGGTTGGGCAAC 16
Db 448 TTTGGTTGGGCAAC 461

RESULT 27
US-08-961-083-47/c
; Sequence 47, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 435
; FILING DATE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-08-961-083-47/c

Query Match 70.0%; Score 14; DB 3; Length 1194;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTGGTTGGGCAAC 16
Db 448 TTTGGTTGGGCAAC 461

RESULT 27
US-08-961-083-47/c
; Sequence 47, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; FILING DATE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-08-961-083-47/c

Query Match 70.0%; Score 14; DB 3; Length 1194;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTGGTTGGGCAAC 16
Db 448 TTTGGTTGGGCAAC 461

RESULT 27
US-08-961-083-47/c
; Sequence 47, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; FILING DATE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-08-961-083-47/c
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1279 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-083-47

Query Match 70.0%; Score 14; DB 3; Length 1279;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTGGTTGGGCAAC 16
Db 273 TTTGGTTGGGCAAC 260

RESULT 28
US-09-536-784-47/c
; Sequence 47, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1279 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-536-784-47

Query Match 70.0%; Score 14; DB 3; Length 1279;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTGGTTGGGCAAC 16
Db 273 TTTGGTTGGGCAAC 260

RESULT 29
US-09-765-271-47/c
; Sequence 47, Application US/09765271
; Patent No. 6887663
; GENERAL INFORMATION:
```

```
;
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,271
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/536,784
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
;
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1279 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-765-271-47

      Query Match          70.0%; Score 14; DB 3; Length 1279;
      Best Local Similarity 100.0%; Pred. No. 47;
      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TTTGGTTGGCAAC 16
Db      273 TTTGGTTGGCAAC 260

RESULT 30
US-09-765-272A-47/C
; Sequence 47, Application US/09765272A
; Patent No. 6929930
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and
; Vaccines
; NUMBER OF SEQUENCES: 454
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: Dell Latitude C610
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272A
; FILING DATE: 22-Jan-2001
```

```
;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin J. Hymel
; REGISTRATION NUMBER: 45,414
; REFERENCE/DOCKET NUMBER: PB340P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 610-5790
; TELEFAX: (301) 309-8439
;
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1279 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-765-272A-47

      Query Match          70.0%; Score 14; DB 3; Length 1279;
      Best Local Similarity 100.0%; Pred. No. 47;
      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TTTGGTTGGCAAC 16
Db      273 TTTGGTTGGCAAC 260

RESULT 31
US-09-196-857-1/C
; Sequence 1, Application US/09196857A
; Patent No. 6100069
; GENERAL INFORMATION:
; APPLICANT: Zalacain, Magdalena
; APPLICANT: Brown, James R.
; APPLICANT: Biswas, Sanjoy
; APPLICANT: Throup, John P.
; APPLICANT: Lawlor, Elizabeth J.
; APPLICANT: Mooney, Jeffrey
; APPLICANT: Zhong, Yiyi
; APPLICANT: Debouck, Christine
; APPLICANT: Jaworski, Deborah D.
; APPLICANT: Wang, Min
; APPLICANT: Warren, Richard L.
; APPLICANT: Schilling, Lisa K.
; TITLE OF INVENTION: No. 6100069el tig
; FILE REFERENCE: GM10118
; CURRENT APPLICATION NUMBER: US/09/196,857A
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: 60/082,418
; EARLIER FILING DATE: 1997-11-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1281)
US-09-196-857-1

      Query Match          70.0%; Score 14; DB 3; Length 1284;
      Best Local Similarity 100.0%; Pred. No. 47;
      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TTTGGTTGGCAAC 16
Db      275 TTTGGTTGGCAAC 262

RESULT 32
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```
US-09-583-110-1279/c
; Sequence 1279, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: Pneumoniae for Diagnostics and Therapeutics
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1279
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1279

Query Match          70.0%; Score 14; DB 3; Length 1284;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TTTGGTTGGGCAAC 16
      |||||
Db      275 TTTGGTTGGGCAAC 262

RESULT 33
US-09-107-433-1653/c
; Sequence 1653, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1653:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1308 base pairs
; TYPE: nucleic acid
; . . .
```

```
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...1308
; SEQUENCE DESCRIPTION: SEQ ID NO: 1653:
US-09-107-433-1653

Query Match          70.0%; Score 14; DB 3; Length 1308;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TTTGGTTGGGCAAC 16
      |||||
Db      299 TTTGGTTGGGCAAC 286

RESULT 34
US-09-917-254-22/c
; Sequence 22, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1449
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (1316)..(1316)
; OTHER INFORMATION: n = a, c, g, or t
; NAME/KEY: Unsure
; LOCATION: (1360)..(1360)
; OTHER INFORMATION: n = a, c, g, or t
; NAME/KEY: Unsure
; LOCATION: (1366)..(1367)
; OTHER INFORMATION: n = a, c, g, or t
; NAME/KEY: Unsure
; LOCATION: (1369)..(1369)
; OTHER INFORMATION: n = a, c, g, or t
US-09-917-254-22

Query Match          70.0%; Score 14; DB 3; Length 1449;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TTTGGTTGGGCAAC 16
      |||||
Db      1429 TTTGGTTGGGCAAC 1416

RESULT 35
US-09-949-016-4402/c
; Sequence 4402, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```



FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 4402  
LENGTH: 2184  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-4402

Query Match 70.0%; Score 14; DB 3; Length 2184;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAACAC 18  
|||||  
DB 1094 TGGTTGGGCAACAC 1081

RESULT 36  
US-08-396-479B-3  
Sequence 3, Application US/08396479B  
Patent No. 5612455  
GENERAL INFORMATION:  
APPLICANT: HOEY, Timothy  
TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING ASSAY  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/396,479B  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: A-59450-1/RAO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 494-8700  
TELEFAX: (415) 494-8771  
TELEX: 210 277299

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2743 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 240..2390  
US-08-396-479B-3

Query Match 70.0%; Score 14; DB 2; Length 2743;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAACAC 18  
|||||  
DB 1137 TGGTTGGGCAACAC 1150

RESULT 37  
US-08-818-823-3  
Sequence 3, Application US/08818823  
Patent No. 5708158  
GENERAL INFORMATION:  
APPLICANT: HOEY, Timothy  
TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING ASSAY  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/818,823  
FILING DATE: 14-MAR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/396,479  
FILING DATE: 02-MAR-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: A-59450-1/RAO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 494-8700  
TELEFAX: (415) 494-8771  
TELEX: 210 277299  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2743 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:

NAME/KEY: CDS  
LOCATION: 240..2390  
US-08-818-823-3

Query Match 70.0%; Score 14; DB 2; Length 2743;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAACAC 18  
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DB 1137 TGGTTGGGCAACAC 1150

RESULT 38  
US-08-124-981A-1  
Sequence 1, Application US/08124981A  
Patent No. 5837840  
GENERAL INFORMATION:  
APPLICANT: Crabtree, Gerald R.  
APPLICANT: No. 5837840throp, Jeffrey P.  
TITLE OF INVENTION: NF-AT POLYPEPTIDES AND POLYNUCLEOTIDES  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/124,981A  
FILING DATE: 20-SEP-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 5490A-226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2749 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 103..2385  
US-08-124-981A-1

Query Match 70.0%; Score 14; DB 2; Length 2749;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGGTTGGGCAACAC 18  
|||||  
Db 1135 TGGTTGGGCAACAC 1148

RESULT 39  
US-09-037-190-45  
Sequence 45, Application US/09037190  
Patent No. 6096515  
GENERAL INFORMATION:  
APPLICANT: Crabtree, Gerald R.  
APPLICANT: No. 6096515throp, Jeffrey P.  
APPLICANT: Ho, Steffan M.  
TITLE OF INVENTION: NF-AT POLYPEPTIDES AND POLYNUCLEOTIDES  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/037,190  
FILING DATE: 09-MAR-1998  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,174  
FILING DATE: 13-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,981

FILING DATE: 20-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: APV-332.03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2751 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 240..2387  
US-09-037-190-45  
Query Match 70.0%; Score 14; DB 3; Length 2751;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 TGGTTGGGCAACAC 18  
|||||  
Db 1137 TGGTTGGGCAACAC 1150  
RESULT 40  
US-09-037-192-45  
Sequence 45, Application US/09037192  
Patent No. 6096860  
GENERAL INFORMATION:  
APPLICANT: Crabtree, Gerald R.  
APPLICANT: No. 6096860throp, Jeffrey P.  
APPLICANT: Ho, Steffan M.  
TITLE OF INVENTION: NF-AT POLYPEPTIDES AND POLYNUCLEOTIDES  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/037,192  
FILING DATE: 09-MAR-1998  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,174  
FILING DATE: 13-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,981  
FILING DATE: 20-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: APV-332.04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2751 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 240..2387
US-09-037-192-45

Query Match
Best Local Similarity 70.0%; Score 14; DB 3; Length 2751;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGGTTGGGCAACAC 18
Db 1137 TGGTTGGGCAACAC 1150

RESULT 41
US-09-037-143-45
; Sequence 45, Application US/09037143A
; Patent No. 6150099
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: No. 6150099throp, Jeffrey P.
; TITLE OF INVENTION: NF-AT POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: APV-332.05
; CURRENT APPLICATION NUMBER: US/09/037,143A
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 2751
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (240)..(2387)
US-09-037-143-45

Query Match
Best Local Similarity 70.0%; Score 14; DB 3; Length 2751;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGGTTGGGCAACAC 18
Db 1137 TGGTTGGGCAACAC 1150

RESULT 42
US-09-049-691-45
; Sequence 45, Application US/09049691
; Patent No. 6171781
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: No. 617178throp, Jeffrey P.
; TITLE OF INVENTION: NF-AT POLYPEPTIDES AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/049,691
; FILING DATE: 27-MAR-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,174
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,981
; FILING DATE: 20-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: APV-332.09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 240..2387
US-09-049-691-45

Query Match
Best Local Similarity 70.0%; Score 14; DB 3; Length 2751;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGGTTGGGCAACAC 18
Db 1137 TGGTTGGGCAACAC 1150

RESULT 43
US-08-260-174-45
; Sequence 45, Application US/08260174C
; Patent No. 6197925
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: No. 6197925throp, Jeffrey P.
; TITLE OF INVENTION: NF-AT POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: APV-332.02
; CURRENT APPLICATION NUMBER: US/08/260,174C
; CURRENT FILING DATE: 1994-06-13
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 2751
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (240)..(2387)
US-08-260-174-45

Query Match
Best Local Similarity 70.0%; Score 14; DB 3; Length 2751;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGGTTGGGCAACAC 18
Db 1137 TGGTTGGGCAACAC 1150

RESULT 44
US-09-338-128A-45

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; Sequence 45, Application US/09338128A  
; Patent No. 6312899  
; GENERAL INFORMATION:  
; APPLICANT: Crabtree, Gerald R.  
; APPLICANT: No. 6312899throp, Jeffrey P.  
; APPLICANT: Ho, Steffan M.  
; TITLE OF INVENTION: NF-AT POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: APV-33211  
; CURRENT APPLICATION NUMBER: US/09/338,128A  
; CURRENT FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: 08/260,174  
; PRIOR FILING DATE: 1994-06-13  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 45  
; LENGTH: 2751  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (240)..(2387)  
US-09-338-128A-45

Query Match 70.0%; Score 14; DB 3; Length 2751;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGGTTGGGCAACAC 18  
Db 1137 TGGTTGGGCAACAC 1150

RESULT 45  
US-09-037-192-45  
; Sequence 45, Application US/09037192  
; Patent No. 6388052  
; GENERAL INFORMATION:  
; APPLICANT: Crabtree, Gerald R.  
; Ho, Steffan M.  
; TITLE OF INVENTION: NF-AT POLYPEPTIDES AND POLYNUCLEOTIDES  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/037,192  
; FILING DATE: 09-Mar-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,174  
; FILING DATE: 13-JUN-1994  
; APPLICATION NUMBER: US 08/124,981  
; FILING DATE: 20-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: APV-332.04  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2751 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 240..2387  
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
US-09-037-192-45

Query Match 70.0%; Score 14; DB 3; Length 2751;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGGTTGGGCAACAC 18  
Db 1137 TGGTTGGGCAACAC 1150

RESULT 46  
PCT-US94-07297-36  
; Sequence 36, Application PC/TUS9407297  
; GENERAL INFORMATION:  
; APPLICANT: Arai, Naoko  
; APPLICANT: Masuda, Eateban S.  
; APPLICANT: Tokumitsu, Hiroshi  
; TITLE OF INVENTION: PURIFIED COMPONENTS OF MAMMALIAN  
; TITLE OF INVENTION: TRANSCRIPTION REGULATION COMPLEXES, AND ANALOGS  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John H. C. Blasdale, Schering-Plough Corporation, M-3-W  
; STREET: One Giralda Farms  
; CITY: Madison  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07940-1000  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh IICx  
; OPERATING SYSTEM: System Software 7.1  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07297  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/222,626  
; FILING DATE: 04-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/148,061  
; FILING DATE: 05-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/113,971  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/099,998  
; FILING DATE: 30-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/088,483  
; FILING DATE: 06-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Blasdale, John H. C.  
; REGISTRATION NUMBER: 31,895  
; REFERENCE/DOCKET NUMBER: DX0392K4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-822-7398  
; TELEFAX: 201-822-7039  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2853 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

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; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 340...2490
PCT-US94-07297-36

Query Match      70.0%; Score 14; DB 6; Length 2853;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAACAC 18
Db 1237 TGGTTGGGCAACAC 1250

RESULT 47
US-09-949-016-823
; Sequence 823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 823
; LENGTH: 2935
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-823

Query Match      70.0%; Score 14; DB 3; Length 2935;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAACAC 18
Db 934 TGGTTGGGCAACAC 947

RESULT 48
US-09-220-132-68
; Sequence 68, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shvlian, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 3082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-68

Query Match      70.0%; Score 14; DB 3; Length 3082;
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Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACACAT 20
Db 406 GTTGGGCAACACAT 419

RESULT 49
US-09-540-236-1660
; Sequence 1660, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1660
; LENGTH: 4152
; TYPE: DNA
; ORGANISM: M. catarrhalis
US-09-540-236-1660

Query Match      70.0%; Score 14; DB 3; Length 4152;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTGGTTGGGCAAC 16
Db 3438 TTTGGTTGGGCAAC 3451

RESULT 50
US-09-949-016-5322
; Sequence 5322, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5322
; LENGTH: 4464
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5322

Query Match      70.0%; Score 14; DB 3; Length 4464;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAACAC 18
Db 1091 TGGTTGGGCAACAC 1104

Search completed: May 6, 2006, 17:19:57
Job time : 129 secs
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GenCore version 5.1.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 00:46:02 ; Search time 1768 Seconds  
(without alignments)  
643.025 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20

Sequence: 1 gcttgggtggcaacacat 20

Scoring table: OLIGO\_NUC

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Searched: 5883141 seqs, 28421725653 residues

Word size : 1

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_pro.\*
- 10: gb\_sts.\*
- 11: gb\_sy.\*
- 12: gb\_un.\*
- 13: gb\_vi.\*
- 14: gb\_htg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	20	100.0	254	6 AX229886	Sequence
C 3	20	100.0	303	6 C0679217	Sequence
C 4	20	100.0	447	6 C0690723	Sequence
C 5	20	100.0	578	6 AX778044	Sequence
C 6	20	100.0	1968	8 BT007455	Homo sapi
C 7	20	100.0	1968	11 AY890173	Synthetic
C 8	20	100.0	1968	11 AY890174	Synthetic
C 9	20	100.0	2103	9 AF126056	Sequence
C 10	20	100.0	2162	4 AY094061	Sus scrofa
C 11	20	100.0	2413	8 BC021981	Homo sapi
C 12	20	100.0	2460	9 AF114258	Sequence
C 13	20	100.0	2482	8 BC070065	Sequence
C 14	20	100.0	2503	9 AY255525	Spermophi
C 15	20	100.0	2725	11 AF178854	Synthetic
C 16	20	100.0	3200	8 H5U02368	Human PAX3/
C 17	20	100.0	3421	6 C0874011	Sequence
C 18	20	100.0	3421	8 H5U02310	Human fork

C 19	20	100.0	3517	8 H5U02308	Human PAX-3
C 20	20	100.0	4714	6 CQ724998	Sequence
C 21	20	100.0	4919	8 H5M808426	Homo sapi
C 22	20	100.0	4945	9 NMU252157	Mus muscu
C 23	20	100.0	5723	6 CS031181	Sequence
C 24	20	100.0	5723	6 CS040133	Sequence
C 25	20	100.0	5723	6 AX587664	Sequence
C 26	20	100.0	5723	8 AF032885	Homo sapi
C 27	20	100.0	5769	6 AX779990	Sequence
C 28	20	100.0	81862	8 AL133318	Human DNA
C 29	20	100.0	149841	14 AC163092	Mus muscu
C 30	20	100.0	155595	14 AC078964	Homo sapi
C 31	20	100.0	186044	14 AC084099	Homo sapi
C 32	20	100.0	228076	14 AC089851	Rattus no
C 33	20	100.0	303046	14 AC113811	Rattus no
C 34	19	95.0	110000	1 AE016828.11	Continuation (12 o
C 35	17	85.0	299	15 AJ834861	Arabidops
C 36	17	85.0	2000	6 AX509544	Sequence
C 37	17	85.0	7618	5 AF537216	Sequence
C 38	17	85.0	40406	5 FRIGVH1	Takifugu
C 39	17	85.0	78423	15 AB024035	Fugu rubr
C 40	17	85.0	110000	1 CP000084.08	Arabidops
C 41	16	80.0	47740	1 AY144116	Continuation (9 of
C 42	16	80.0	105083	14 AC095920.09	Photorhab
C 43	16	80.0	110000	15 AP008214.026	Continuation (10 o
C 44	16	80.0	139455	8 AC097534	Continuation (27 o
C 45	16	80.0	141257	15 AP005741	Homo sapi
C 46	16	80.0	154612	14 AC093739	Oryza sat
C 47	16	80.0	160625	8 AC009311	AC093739 Homo sapi
C 48	16	80.0	166472	14 AC009588	Homo sapi
C 49	16	80.0	188776	9 BX537258	AC009588 Homo sapi
C 50	16	80.0	193506	9 AC116953	Mouse DNA
C 51	16	80.0	221363	5 BX005389	Mus muscu
C 52	16	80.0	239627	14 AC152177	Zebracfish
C 53	16	80.0	250128	14 AC162246	AC152177 Medicago
C 54	16	80.0	255453	14 AC109391	Bos tauru
C 55	16	80.0	261001	14 AC096324	Rattus no
C 56	16	80.0	280615	14 AC096297	Rattus no
C 57	15	75.0	406	1 AF536051	Haemophil
C 58	15	75.0	406	1 AF536052	Haemophil
C 59	15	75.0	406	1 AF536053	Haemophil
C 60	15	75.0	406	1 AF536054	Haemophil
C 61	15	75.0	406	1 AF536055	Haemophil
C 62	15	75.0	406	1 AF536056	Haemophil
C 63	15	75.0	406	1 AF536057	Haemophil
C 64	15	75.0	406	1 AF536058	Haemophil
C 65	15	75.0	406	1 AF536059	Haemophil
C 66	15	75.0	406	1 AF536060	Haemophil
C 67	15	75.0	406	1 AF536061	Haemophil
C 68	15	75.0	406	1 AF536062	Haemophil
C 69	15	75.0	406	1 AF536063	Haemophil
C 70	15	75.0	406	1 AF536064	Haemophil
C 71	15	75.0	406	1 AF536065	Haemophil
C 72	15	75.0	406	1 AF536066	Haemophil
C 73	15	75.0	406	1 AF536067	Haemophil
C 74	15	75.0	406	1 AF536068	Haemophil
C 75	15	75.0	406	1 AF536069	Haemophil
C 76	15	75.0	406	1 AF536070	Haemophil
C 77	15	75.0	579	10 G97533	G97533 S208P567FG
C 78	15	75.0	629	10 BV412283	BV412283 S229P668F
C 79	15	75.0	703	8 H5A328477	Homo sapi
C 80	15	75.0	714	15 AF482832	Agaricus
C 81	15	75.0	756	10 BV624260	BV624260 S215P6161
C 82	15	75.0	817	10 BV665156	BV665156 S216P6206
C 83	15	75.0	1342	6 BD195279	BD195279 Nucleotid
C 84	15	75.0	1342	6 AB580476	AB580476 Sequence
C 85	15	75.0	1413	6 CQ739385	CQ739385 Sequence
C 86	15	75.0	1513	8 BC062359	BC062359 Homo sapi
C 87	15	75.0	1540	15 D89249	D89249 Schistosacch
C 88	15	75.0	1550	6 AX834422	AX834422 Sequence
C 89	15	75.0	1550	6 AK096872	AK096872 Homo sapi
C 90	15	75.0	1701	8 AK378624	AK378624 Sequence
C 91	15	75.0	1758	9 BC034067	BC034067 Mus muscu

C	92	15	75.0	1758	9	BC040758	Mus muscu	C 165	15	75.0	156007	8	HSB4425A6	AL121749	Human DNA
	93	15	75.0	2181	6	AR321439	Sequence	C 166	15	75.0	166518	8	AC090514	AC090514	Homo sapi
	94	15	75.0	2550	6	BD156870	Primer fo	C 167	15	75.0	168362	9	AC119228	AC119228	Mus muscu
	95	15	75.0	2550	6	AX877826	Sequence	C 168	15	75.0	168587	8	AP003439	AP003439	Homo sapi
	96	15	75.0	2550	8	AK027803	Homo sapi	C 169	15	75.0	169077	8	AC066613	AC066613	Homo sapi
	97	15	75.0	3059	6	AX714232	Sequence	C 170	15	75.0	170233	15	AC135418	AC135418	Oryza sat
	98	15	75.0	3059	8	AK056441	Homo sapi	C 171	15	75.0	171113	14	AC034266	AC034266	Homo sapi
	99	15	75.0	3342	6	CQ604796	Sequence	C 172	15	75.0	171962	14	AC013537	AC013537	Homo sapi
	100	15	75.0	3366	6	CQ595320	Sequence	C 173	15	75.0	173814	8	AC093840	AC093840	Homo sapi
C	101	15	75.0	3416	2	AF181657	AF181657	C 174	15	75.0	174376	2	AC092230	AC092230	Drosophil
	102	15	75.0	3593	6	CQ777454	Sequence	C 175	15	75.0	175461	14	AC163768	AC163768	Pan trogl
	103	15	75.0	3593	6	AR592428	Sequence	C 176	15	75.0	175488	14	AC013556	AC013556	Homo sapi
	104	15	75.0	3593	6	AX088418	Sequence	C 177	15	75.0	177187	14	AC096848	AC096848	Paplo ann
	105	15	75.0	3593	6	AX088429	Sequence	C 178	15	75.0	177242	14	AC021923	AC021923	Homo sapi
	106	15	75.0	3593	9	AF233517	Mus muscu	C 179	15	75.0	178348	14	AC132931	AC132931	Mus muscu
C	107	15	75.0	3697	9	BC066841	Mus muscu	C 180	15	75.0	179060	14	AC074382	AC074382	Homo sapi
	108	15	75.0	4529	6	CQ728565	Sequence	C 181	15	75.0	179080	14	AC092514	AC092514	Paplo ann
	109	15	75.0	5128	8	AF525401	Homo sapi	C 182	15	75.0	179485	8	AC095939	AC095939	Homo sapi
	110	15	75.0	5205	8	AR487565	Sequence	C 183	15	75.0	183773	9	AC154213	AC154213	Mus muscu
	111	15	75.0	5250	8	AY061886	Homo sapi	C 184	15	75.0	184650	14	AC161833	AC161833	Bos tauru
	112	15	75.0	5492	6	CQ595319	Sequence	C 185	15	75.0	185137	5	AL954187	AL954187	Zebrafish
C	113	15	75.0	6308	6	AR487554	Sequence	C 186	15	75.0	185583	9	AC153553	AC153553	Mus muscu
	114	15	75.0	12000	5	UA3315159	U3315159 Xenopus l	C 187	15	75.0	187349	8	AP003352	AP003352	Homo sapi
	115	15	75.0	12361	1	XJ2787	Caenorhabdi	C 188	15	75.0	188177	9	AC121135	AC121135	Mus muscu
	116	15	75.0	28469	2	U80033	U80033	C 189	15	75.0	188764	14	AC021238	AC021238	Homo sapi
	117	15	75.0	23733	15	MAPEFSYNT	X89442 Metarhizium	C 190	15	75.0	192649	9	AC161805	AC161805	Mus muscu
C	118	15	75.0	47079	14	AC083776	AC083776	C 191	15	75.0	193265	14	AC127443	AC127443	Rattus no
	119	15	75.0	53881	14	AP007990	AP007990 Lotus cor	C 192	15	75.0	194834	9	AC119864	AC119864	Mus muscu
C	120	15	75.0	62198	5	AJ621739	AJ621739 Gallus ga	C 193	15	75.0	196208	9	AC134426	AC134426	



238	15	75.0	245938	14	AC127850	AC127850 Rattus no	c 311	14	70.0	1284	6	BD138852	BD138852 Novel TIG
239	15	75.0	246237	2	CEY13986A	AL132948 Caenorhab	c 312	14	70.0	1284	6	AR480375	AR480375 Sequence
c 240	15	75.0	248808	14	AC163808	AL132948 Bos taurus	c 313	14	70.0	1308	6	AR587534	AR587534 Sequence
c 241	15	75.0	249412	14	AC095097	AC095097 Rattus no	c 314	14	70.0	1349	6	CQ727045	CQ727045 Sequence
c 242	15	75.0	255090	14	AC098334	AC098334 Rattus no	c 315	14	70.0	1447	6	BC043286	BC043286 Homo sapi
c 243	15	75.0	259718	2	AE003614	AE003614 Drosophila	c 316	14	70.0	1448	8	HUMEL20	M17282 Human elast
c 244	15	75.0	260657	14	AC094371	AC094371 Rattus no	c 317	14	70.0	1449	6	AR482463	AR482463 Sequence
245	15	75.0	261918	14	AC145000	AC145000 Gorilla g	c 318	14	70.0	1449	6	AX375019	AX375019 Sequence
246	15	75.0	267191	14	AC132043	AC132043 Rattus no	c 319	14	70.0	1449	8	HSU77846	U77846 Human elast
247	15	75.0	270873	14	AC118304	AC118304 Rattus no	c 320	14	70.0	1450	15	BT009143	BT009143 Triticum
248	15	75.0	273105	14	AC112439	AC112439 Rattus no	c 321	14	70.0	1516	2	AB052887	AB052887 Oryza sat
c 249	15	75.0	274839	14	AC105653	AC105653 Rattus no	c 322	14	70.0	1522	2	AK113053	AK113053 Ciona int
c 250	15	75.0	274906	14	AC094962	AC094962 Rattus no	c 323	14	70.0	1625	15	AB033537	AB033537 Oryza sat
251	15	75.0	293044	14	AC106112	AC106112 Rattus no	c 324	14	70.0	1653	15	AK061762	AK061762 Oryza sat
252	15	75.0	298060	14	AC136133	AC136133 Rattus no	c 325	14	70.0	1653	15	AK106217	AK106217 Oryza sat
253	15	75.0	315480	14	AC163184	AC163184 Bos taurus	c 326	14	70.0	1663	2	AF227504	AF227504 Trypanoso
c 254	15	75.0	349571	9	BM883047	BM883047 Rattus no	c 327	14	70.0	1772	15	AK102286	AK102286 Oryza sat
255	15	75.0	349688	1	CR378671	CR378671 Photobact	328	14	70.0	1922	9	BC028893	BC028893 Mus muscu
256	15	75.0	349980	6	C0873072	C0873072 Sequence	329	14	70.0	1935	8	HUMBLNDC	L10405 Homo sapien
c 257	14	70.0	88	6	AX645238	AX645238 Sequence	330	14	70.0	2010	9	BC002283	BC002283 Mus muscu
c 258	14	70.0	88	6	AX676399	AX676399 Sequence	331	14	70.0	2046	8	CS000989	CS000989 Sequence
c 259	14	70.0	131	5	ONHAP0A11	L49426 Oncorhynch	c 332	14	70.0	2055	6	CQ750982	CQ750982 Sequence
c 260	14	70.0	131	5	SMOAP0A1B	L49424 Salmo trutt	333	14	70.0	2064	11	CS000995	CS000995 Sequence
c 261	14	70.0	131	5	SMOIVS11	L49413 Salmo salar	334	14	70.0	2097	6	BD105250	BD105250 New enzym
c 262	14	70.0	190	15	AF308853S2	AF308854 Lotus cor	335	14	70.0	2097	6	BD134620	BD134620 Novel enz
c 263	14	70.0	306	6	CQ601509	CQ601509 Sequence	336	14	70.0	2100	8	CS000993	CS000993 Sequence
c 264	14	70.0	330	10	BV424911	BV424911 S237P6442	c 337	14	70.0	2116	5	RCALN	U03471 Rana cateab
265	14	70.0	339	6	CQ434837	CQ434837 Sequence	338	14	70.0	2118	11	CS000999	CS000999 Sequence
266	14	70.0	349	6	BD046419	BD046419 Sequence	339	14	70.0	2118	15	ZMA558238	AJ5558238 Zea mays
c 267	14	70.0	349	6	AX910886	AX910886 Sequence	340	14	70.0	2129	6	AX710574	AX710574 Sequence
c 268	14	70.0	387	6	CQ689047	CQ689047 Sequence	341	14	70.0	2170	6	AX821985	AX821985 Sequence
269	14	70.0	410	6	BR209605	BR209605 Compositi	c 342	14	70.0	2197	8	HSPFLZFA	Z19002 H. sapiens o
270	14	70.0	410	6	BR209605	BR209605 Compositi	c 343	14	70.0	2287	8	BC026902	BC026902 Homo sapi
271	14	70.0	519	8	AX441734	AX441734 Propithec	c 344	14	70.0	2299	9	AY781104	AY781104 Rattus no
c 272	14	70.0	616	10	BV224390	BV224390 S233P6187	c 345	14	70.0	2306	6	CQ601508	CQ601508 Sequence
c 273	14	70.0	632	6	CQ525373	CQ525373 Sequence	c 346	14	70.0	2306	9	AY781102	AY781102 Rattus no
274	14	70.0	633	10	BV282791	BV282791 S232P6101	347	14	70.0	2328	8	AK027010	AK027010 Homo sapi
c 275	14	70.0	647	10	BV411642	BV411642 S229P6500	c 348	14	70.0	2331	9	AY781103	AY781103 Rattus no
c 276	14	70.0	657	6	BD149967	BD149967 Primer fo	c 349	14	70.0	2374	8	BC029812	BC029812 Homo sapi
c 277	14	70.0	657	6	AX869905	AX869905 Sequence	c 350	14	70.0	2407	6	CQ489441	CQ489441 Sequence
c 278	14	70.0	707	6	AR212646	AR212646 Sequence	c 351	14	70.0	2407	6	CQ491775	CQ491775 Sequence
279	14	70.0	707	6	AR590687	AR590687 Sequence	c 352	14	70.0	2407	6	CQ495283	CQ495283 Sequence
280	14	70.0	712	10	BV512539	BV512539 qzt31c05.	c 353	14	70.0	2407	6	CQ497666	CQ497666 Sequence
281	14	70.0	715	15	AF485197	AF485197 Begonia v	c 354	14	70.0	2410	5	GGDLCA	X79088 G.gallus mR
c 282	14	70.0	718	8	HA339001	AX339001 Homo sapi	355	14	70.0	2439	6	AX695613	AX695613 Sequence
283	14	70.0	723	6	AX829066	AX829066 Sequence	356	14	70.0	2439	15	DQ116825	DQ116825 Saccharom
c 284	14	70.0	737	10	BV529703	BV529703 G591P6176	357	14	70.0	2493	15	DQ116826	DQ116826 Saccharom
c 285	14	70.0	748	3	AF349989	AF349989 Unculture	358	14	70.0	2493	15	DQ116827	DQ116827 Saccharom
286	14	70.0	750	1	DR2966	DR2966 Shigella fl	359	14	70.0	2493	15	DQ116828	DQ116828 Saccharom
287	14	70.0	753	3	AF349978	AF349978 Unculture	c 360	14	70.0	2510	8	HSM809124	BM648973 Homo sapi
288	14	70.0	753	3	AF349984	AF349984 Unculture	361	14	70.0	2541	9	S78773	S78773 musfiblp-fi
289	14	70.0	753	3	AF349985	AF349985 Unculture	362	14	70.0	2541	15	SCYNL084C	271360 S. cerevisia
290	14	70.0	757	3	AF349976	AF349976 Unculture	363	14	70.0	2743	6	BD094063	BD094063 Shear str
c 291	14	70.0	761	10	BV556507	BV556507 S222P6162	364	14	70.0	2743	6	I38153	I38153 Sequence 3
c 292	14	70.0	771	8	HA333758	HA333758 Homo sapi	365	14	70.0	2743	6	I80095	I80095 Sequence 3
c 293	14	70.0	792	10	BV544926	BV544926 G591P6060	366	14	70.0	2743	8	HSU08015	HSU08015 Human NF-AT
c 294	14	70.0	825	6	AX829064	AX829064 Sequence	367	14	70.0	2749	6	AR058939	AR058939 Sequence
c 295	14	70.0	864	15	AF475120	AF475120 Triticum	368	14	70.0	2749	6	AX469982	AX469982 Sequence
296	14	70.0	924	10	BV096731	BV096731 BARC0074	369	14	70.0	2751	6	AR105239	AR105239 Sequence
c 297	14	70.0	933	9	AX317988	AX317988 Mus muscu	370	14	70.0	2751	6	AR119160	AR119160 Sequence
c 298	14	70.0	965	10	BV525276	BV525276 G591P6062	371	14	70.0	2751	6	AR123531	AR123531 Sequence
c 299	14	70.0	1002	2	AT095043	AT095043 Drosophila	372	14	70.0	2751	6	AR138184	AR138184 Sequence
300	14	70.0	1083	6	AX829062	AX829062 Sequence	373	14	70.0	2751	6	AR176745	AR176745 Sequence
301	14	70.0	1121	9	AF232725	AF232725 Marmota m	374	14	70.0	2751	6	BD274649	BD274649 NF-AT-med
c 302	14	70.0	1194	1	AY091643	AY091643 Pseudomon	375	14	70.0	2775	6	CQ714412	CQ714412 Sequence
303	14	70.0	1194	6	AR481365	AR481365 Sequence	376	14	70.0	2793	6	AX710565	AX710565 Sequence
304	14	70.0	1194	6	AR586175	AR586175 Sequence	377	14	70.0	2935	6	AX695612	AX695612 Sequence
c 305	14	70.0	1275	6	AX653352	AX653352 Sequence	378	14	70.0	2935	8	HSU59736	HSU59736 Human trans
c 306	14	70.0	1279	6	AR120261	AR120261 Sequence	379	14	70.0	2994	15	SCU09129	SCU09129 Sequence
c 307	14	70.0	1279	6	AR340952	AR340952 Streptoco	380	14	70.0	3082	6	AR274931	AR274931 Saccharomyc
c 308	14	70.0	1279	6	AR340952	AR340952 Sequence	381	14	70.0	3082	8	HUMGPAT	M90516 Human gluta
c 309	14	70.0	1279	6	AR653215	AR653215 Sequence	382	14	70.0	3082	10	G28527	G28527 human STS S
c 310	14	70.0	1281	6	AX567439	AX567439 Sequence	383	14	70.0	3140	6	CS032680	CS032680 Sequence

384	14	70.0	3140	6	CS041632 Sequence	457	14	70.0	42017	14	AC147080	AC147080 Homo sapi
385	14	70.0	3160	8	BC045641 Homo sapi	458	14	70.0	45349	8	AC011525	AC011525 Homo sapi
386	14	70.0	3295	9	MUSF1BLP2	c 459	14	70.0	45626	14	AY207045	AY207045 Homo sapi
387	14	70.0	3349	15	AK066418	c 460	14	70.0	48787	15	DQ115393	DQ115393 Saccharom
388	14	70.0	3402	15	SCYNL085W	461	14	70.0	50701	1	CP000661	Continuation (27 o
c 389	14	70.0	3710	9	RNU66878	462	14	70.0	50927	6	CQ869661	Sequence
390	14	70.0	3803	15	AK055064	c 463	14	70.0	52284	8	CH19R25187	AD000685 Homo sapi
391	14	70.0	4152	6	AR450996	c 464	14	70.0	53157	8	AL136302	AL136302 Human DNA
c 392	14	70.0	4169	6	C0612380	c 465	14	70.0	54425	8	AC095352	AC095352 Homo sapi
c 393	14	70.0	4278	5	BC058830	c 466	14	70.0	58348	14	AC144883	AC144883 Papio anu
c 394	14	70.0	4350	15	AF432498	c 467	14	70.0	60886	8	AL591969	AL591969 Human DNA
c 395	14	70.0	4427	8	AB208916	c 468	14	70.0	61021	14	AC101916	AC101916 Mus muscu
c 396	14	70.0	4539	6	AR576998	c 469	14	70.0	62370	14	AL451008	AL451008 Homo sapi
c 397	14	70.0	4539	6	AX135962	470	14	70.0	62377	14	AL360009	AL360009 Homo sapi
c 398	14	70.0	4539	6	BD015022	471	14	70.0	63062	14	AC135057	AC135057 Homo sapi
399	14	70.0	4617	8	HSU08018	c 472	14	70.0	63062	14	AC135057	AC135057 Homo sapi
400	14	70.0	4678	8	HSU080917	c 473	14	70.0	63981	14	AC139146	AC139146 Homo sapi
401	14	70.0	5030	6	CQ591719	c 474	14	70.0	63981	14	AC139146	AC139146 Homo sapi
402	14	70.0	5358	6	CQ585377	c 475	14	70.0	65194	14	AC111098	AC111098 Mus muscu
403	14	70.0	5403	6	BD062061	c 476	14	70.0	66082	14	AC109316	AC109316 Homo sapi
404	14	70.0	5403	6	AR212643	c 477	14	70.0	66129	8	AP000281	AP000281 Homo sapi
405	14	70.0	5403	6	AR590684	c 478	14	70.0	67046	8	HSU63721	U63721 Human elast
406	14	70.0	5403	9	AF025818	c 479	14	70.0	67598	14	AC124282	AC124282 Homo sapi
c 407	14	70.0	5419	14	AC018287	c 480	14	70.0	68491	5	AJ621744	AJ621744 Gallus ga
408	14	70.0	5502	6	AR198316	c 481	14	70.0	68548	8	HSU70984	U70984 Human Xp22
409	14	70.0	5502	6	AR648968	c 482	14	70.0	68984	14	AC101203	AC101203 Mus muscu
c 410	14	70.0	5865	8	HS1ZF1	c 483	14	70.0	69411	15	AP004898	AP004898 Lotus cor
c 411	14	70.0	6827	13	AF238884	c 484	14	70.0	74007	14	AC101438	AC101438 Mus muscu
c 412	14	70.0	7356	15	AY191830	c 485	14	70.0	75430	14	AC166182	AC166182 Bos tauru
c 413	14	70.0	8002	6	CQ585590	c 486	14	70.0	76177	14	AC021620	AC021620 Homo sapi
414	14	70.0	8438	4	BTY17260	c 487	14	70.0	77138	14	AC025299	AC025299 Homo sapi
415	14	70.0	10271	1	U32790	c 488	14	70.0	80000	6	CQ819404	CQ819404 Sequence
c 416	14	70.0	10271	6	AX191761	c 489	14	70.0	82288	14	AC164698	AC164698 Bos tauru
c 417	14	70.0	10554	1	AE006778	c 490	14	70.0	82360	2	AC084465	AC084465 Caenorhab
c 418	14	70.0	10819	1	AE007352	c 491	14	70.0	82510	15	AC146328	AC146328 Oryza sat
c 419	14	70.0	10834	1	AE004020	c 492	14	70.0	82818	14	AC012754	AC012754 Drosophil
c 420	14	70.0	10949	1	AE008416	c 493	14	70.0	83684	8	AC105290	AC105290 Homo sapi
421	14	70.0	10966	1	AE015527	c 494	14	70.0	84415	14	AP008177	AP008177 Lotus cor
422	14	70.0	11093	1	AE010132	c 495	14	70.0	84972	8	AL365499	AL365499 Human DNA
c 423	14	70.0	11309	1	AE004051	c 496	14	70.0	85694	15	BX842599	BX842599 Neurospor
c 424	14	70.0	11647	14	AC133648_5	c 497	14	70.0	88823	8	AL713965	AL713965 Human DNA
c 425	14	70.0	14095	8	AC135052	c 498	14	70.0	89328	6	AX329823	AX329823 Sequence
c 426	14	70.0	14283	6	CQ587180	c 499	14	70.0	89328	8	HSJ398C22	Z93784 Human DNA s
427	14	70.0	15564	1	AB185495	c 500	14	70.0	94835	8	HSJ316D7	AL049575 Human DNA
c 428	14	70.0	16995	6	CQ788991	c 501	14	70.0	96013	8	AL353779	AL353779 Human DNA
c 429	14	70.0	16995	6	AR218850	c 502	14	70.0	96597	6	AX695611	AX695611 Sequence
c 430	14	70.0	16995	6	BD003762	c 503	14	70.0	97641	14	AP007792	AP007792 Lotus cor
c 431	14	70.0	17933	15	SCORFSDNA	c 504	14	70.0	98188	8	AC005056	AC005056 Homo sapi
c 432	14	70.0	20866	8	HSU62292	c 505	14	70.0	98935	8	AC004935	AC004935 Homo sapi
c 433	14	70.0	23743	1	AP005325	c 506	14	70.0	99824	14	AC157722	AC157722 Xenopus t
434	14	70.0	24526	6	AX472617	c 507	14	70.0	100000	8	AP000040	AP000040 Homo sapi
435	14	70.0	24965	14	AC014507	c 508	14	70.0	100000	8	AP000108	AP000108 Homo sapi
436	14	70.0	26130	1	AF212041	c 509	14	70.0	100000	8	AP000184	AP000184 Homo sapi
437	14	70.0	27856	1	CG1420072	c 510	14	70.0	100268	14	AC151361	AC151361 Xenopus t
438	14	70.0	31986	15	AF458976	c 511	14	70.0	101172	15	AP006364	AP006364 Lotus cor
439	14	70.0	32051	15	AF458978	c 512	14	70.0	101442	5	AC151340	AC151340 Xenopus t
440	14	70.0	32053	15	AF458981	c 513	14	70.0	104135	8	AC113373	AC113373 Homo sapi
441	14	70.0	32054	15	AF458969	c 514	14	70.0	104729	8	HS118B18	AL034344 Human DNA
442	14	70.0	32055	15	AF458970	c 515	14	70.0	107120	14	AC091831	AC091831 Homo sapi
443	14	70.0	32055	15	AF458975	c 516	14	70.0	107482	15	BX908789	BX908789 Neurospor
444	14	70.0	32055	15	AF458977	c 517	14	70.0	108836	8	AC069137	AC069137 Homo sapi
445	14	70.0	32056	15	AF458980	c 518	14	70.0	110000	1	CR522870_28	Continuation (29 o
446	14	70.0	32057	15	AF458979	c 519	14	70.0	110000	1	CR526927_01	Continuation (2 of
447	14	70.0	32077	15	AF458972	c 520	14	70.0	110000	1	CR626927_02	Continuation (3 of
448	14	70.0	32077	15	AF458974	c 521	14	70.0	110000	1	CR626927_25	Continuation (26 o
449	14	70.0	32078	15	AF458971	c 522	14	70.0	110000	1	AE008692_02	Continuation (3 of
450	14	70.0	32078	15	AF458973	c 523	14	70.0	110000	1	AE009951_08	Continuation (9 of
c 451	14	70.0	34971	8	AP006749	c 524	14	70.0	110000	1	AE016853_37	Continuation (38 o
452	14	70.0	35202	15	AC149413	c 525	14	70.0	110000	1	AE017340_20	Continuation (21 o
453	14	70.0	35484	2	CET26E4	c 526	14	70.0	110000	1	AP006840_01	Continuation (2 of
454	14	70.0	39539	14	AC145113	c 527	14	70.0	110000	1	AP006841_02	Continuation (3 of
c 455	14	70.0	40875	8	AP000702	c 528	14	70.0	110000	1	AP006841_24	Continuation (25 o
c 456	14	70.0	41541	8	AP000703	c 529	14	70.0	110000	1	AP008231_16	Continuation (17 o

c 530	14	70.0	110000	1	BA000019_50	Continuation (51 o	c 603	14	70.0	140597	14	AC148145	AC148145 Canis fam
c 531	14	70.0	110000	1	BA000022_18	Continuation (19 o	c 604	14	70.0	141370	14	AC090798	AC090798 Homo sapi
c 532	14	70.0	110000	1	BA000028_02	Continuation (3 of	c 605	14	70.0	141466	9	AC144817	AC144817 Mus muscu
c 533	14	70.0	110000	1	BA000031_12	Continuation (13 o	c 606	14	70.0	141655	8	HS1093G12	AL121751 Human DNA
c 534	14	70.0	110000	1	BA000035_00	BA000035 Coryneb	c 607	14	70.0	141687	14	AC143315	AC143315 Macaca mu
c 535	14	70.0	110000	1	BA000035_06	Continuation (5 of	c 608	14	70.0	143167	14	AC023976	AC023976 Homo sapi
c 536	14	70.0	110000	1	BA000035_04	Continuation (7 of	c 609	14	70.0	143366	14	AC147004	AC147004 Homo sapi
c 537	14	70.0	110000	1	BA000035_07	Continuation (8 of	c 610	14	70.0	143822	14	AC141668	AC141668 Apis mell
c 538	14	70.0	110000	1	BA000035_12	Continuation (13 o	c 611	14	70.0	144007	14	AC141743	AC141743 Apis mell
c 539	14	70.0	110000	1	BA000035_14	Continuation (15 o	c 612	14	70.0	144728	14	AC152135	AC152135 Dasytus n
c 540	14	70.0	110000	1	BA000035_18	Continuation (19 o	c 613	14	70.0	144734	14	AP001839	AP001839 Homo sapi
c 541	14	70.0	110000	1	BA000035_20	Continuation (21 o	c 614	14	70.0	145294	5	CR354539	CR354539 Zebrafish
c 542	14	70.0	110000	1	BA000035_23	Continuation (24 o	c 615	14	70.0	145722	14	AC152483	AC152483 Dasytus n
c 543	14	70.0	110000	1	BA000035_27	Continuation (28 o	c 616	14	70.0	146455	8	AC127512	AC127512 Homo sapi
c 544	14	70.0	110000	1	BA000038_06	Continuation (7 of	c 617	14	70.0	146575	9	AC127676	AC127676 Mus muscu
c 545	14	70.0	110000	1	CP000040_37	Continuation (38 o	c 618	14	70.0	147514	8	AC008521	AC008521 Homo sapi
c 546	14	70.0	110000	1	CP000075_43	Continuation (44 o	c 619	14	70.0	147739	15	AP005915	AP005915 Oryza sat
c 547	14	70.0	110000	1	CP000082_25	Continuation (26 o	c 620	14	70.0	148090	9	AC100737	AC100737 Mus muscu
c 548	14	70.0	110000	1	CP000089_32	Continuation (33 o	c 621	14	70.0	148419	15	AP004378	AP004378 Oryza sat
c 549	14	70.0	110000	14	AC096113_2	Continuation (3 of	c 622	14	70.0	148683	5	BX248499	BX248499 Zebrafish
c 550	14	70.0	110000	14	AC109084_0	AC109084 Rattus no	c 623	14	70.0	148850	8	AC116622	AC116622 Homo sapi
c 551	14	70.0	110000	14	AC128164_1	Continuation (2 of	c 624	14	70.0	148869	8	AC024093	AC024093 Homo sapi
c 552	14	70.0	110000	14	CR974449_2	Continuation (3 of	c 625	14	70.0	149050	8	AC024697	AC024697 Homo sapi
c 553	14	70.0	110000	14	CT010490_1	Continuation (2 of	c 626	14	70.0	149132	8	AP000908	AP000908 Homo sapi
c 554	14	70.0	110000	14	CT010490_2	Continuation (3 of	c 627	14	70.0	149299	14	AC141832	AC141832 Apis mell
c 555	14	70.0	110000	15	AP008217_006	Continuation (7 of	c 628	14	70.0	149440	14	AC112728	AC112728 Drosophil
c 556	14	70.0	110000	15	AP008217_041	Continuation (42 o	c 629	14	70.0	149461	9	AC117191	AC117191 Mus muscu
c 557	14	70.0	110000	15	AP008217_230	Continuation (231	c 630	14	70.0	150295	15	AC120885	AC120885 Oryza sat
c 558	14	70.0	110000	15	AP008218_007	Continuation (8 of	c 631	14	70.0	151552	14	AC023437	AC023437 Homo sapi
c 559	14	70.0	110000	15	AP008218_263	Continuation (264	c 632	14	70.0	152161	8	AL359074	AL359074 Human DNA
c 560	14	70.0	110000	15	AP008218_263	Continuation (15 o	c 633	14	70.0	152274	14	AC079020	AC079020 Homo sapi
c 561	14	70.0	110000	15	AP008208_059	Continuation (60 o	c 634	14	70.0	153972	5	BX322643	BX322643 Zebrafish
c 562	14	70.0	110000	15	AP008208_312	Continuation (313	c 635	14	70.0	154446	9	AC110513	AC110513 Mus muscu
c 563	14	70.0	110000	15	AP008210_186	Continuation (187	c 636	14	70.0	154446	9	AC110513	AC110513 Mus muscu
c 564	14	70.0	110000	15	AP008211_143	Continuation (144	c 637	14	70.0	155064	8	CNS01DUP	AL133312 Human chr
c 565	14	70.0	110000	15	AP008211_277	Continuation (278	c 638	14	70.0	155168	9	AL683881	AL683881 Mouse DNA
c 566	14	70.0	111135	14	SPENU1906	AL449928 Streptoco	c 639	14	70.0	155332	14	AL365439	AL365439 Homo sapi
c 567	14	70.0	111824	8	AL160412	AL160412 Human DNA	c 640	14	70.0	155375	8	HS914P14	AL031117 Human DNA
c 568	14	70.0	112357	8	AC011378	AC011378 Homo sapi	c 641	14	70.0	155713	5	EX000347	BX000347 Zebrafish
c 569	14	70.0	113474	14	AC013932	AC013932 Drosophil	c 642	14	70.0	156842	14	AC064820	AC064820 Homo sapi
c 570	14	70.0	113778	15	BX897674	BX897674 Neurospil	c 643	14	70.0	157061	8	AC010250	AC010250 Homo sapi
c 571	14	70.0	114233	8	AP000783	AP000783 Homo sapi	c 644	14	70.0	157091	14	AC027772	AC027772 Homo sapi
c 572	14	70.0	115145	9	AL807240	AL807240 Mouse DNA	c 645	14	70.0	157101	8	AC092000	AC092000 Homo sapi
c 573	14	70.0	117273	14	AC015138	AC015138 Drosophil	c 646	14	70.0	157665	8	AC104695	AC104695 Homo sapi
c 574	14	70.0	117411	8	AL590621	AL590621 Human DNA	c 647	14	70.0	157946	8	AL445523	AL445523 Human DNA
c 575	14	70.0	117432	8	AC108704	AC108704 Homo sapi	c 648	14	70.0	158792	15	AP003833	AP003833 Oryza sat
c 576	14	70.0	117724	15	AC104271	AC104271 Oryza sat	c 649	14	70.0	159138	9	AC124403	AC124403 Mus muscu
c 577	14	70.0	118068	8	AL356798	AL356798 Human DNA	c 650	14	70.0	159401	14	CR936468	CR936468 Dario rer
c 578	14	70.0	118211	15	CNS08CE1	EX000511 Oryza sat	c 651	14	70.0	159664	14	AL592441	AL592441 Homo sapi
c 579	14	70.0	120472	8	AC091834	AC091834 Homo sapi	c 652	14	70.0	159802	14	AC019262	AC019262 Homo sapi
c 580	14	70.0	123288	8	AL354712	AL354712 Human DNA	c 653	14	70.0	159984	14	AC162736	AC162736 Loxodonta
c 581	14	70.0	125032	8	AC115286	AC115286 Homo sapi	c 654	14	70.0	160118	14	AC113231	AC113231 Canis fam
c 582	14	70.0	128990	9	AC134436	AC134436 Mus muscu	c 655	14	70.0	160230	9	BX072552	BX072552 Mouse DNA
c 583	14	70.0	130305	14	AL119841	AC119841 Mus muscu	c 656	14	70.0	160341	8	AL161629	AL161629 Human DNA
c 584	14	70.0	130898	8	AL353770	AL353770 Human DNA	c 657	14	70.0	160346	2	AC105578	AC105578 Drosophil
c 585	14	70.0	130910	15	OSJN001132	AL607000 Oryza sat	c 658	14	70.0	160364	9	AC155331	AC155331 Mus muscu
c 586	14	70.0	131689	15	CNS08CB9	AL845347 Oryza sat	c 659	14	70.0	160434	14	AC018998	AC018998 Homo sapi
c 587	14	70.0	133072	14	AC128210	AC128210 Rattus no	c 660	14	70.0	160511	14	AC022786	AC022786 Homo sapi
c 588	14	70.0	133336	15	AC149134	AC149134 Medicago	c 661	14	70.0	160667	14	AC151623	AC151623 Bos tauru
c 589	14	70.0	133978	9	AC155289	AC155289 Mus muscu	c 662	14	70.0	160855	14	AC011579	AC011579 Homo sapi
c 590	14	70.0	133978	15	CNS08CB8P	AL733885 Oryza sat	c 663	14	70.0	160867	8	AC025254	AC025254 Homo sapi
c 591	14	70.0	134205	14	AC145218	AC145218 Medicago	c 664	14	70.0	161153	8	AC020987	AC020987 Homo sapi
c 592	14	70.0	134218	8	AF305872	AF305872 Homo sapi	c 665	14	70.0	161206	14	AC141737	AC141737 Apis mell
c 593	14	70.0	134464	15	AC148373	AC148373 Oryctolag	c 666	14	70.0	161679	8	AL592435	AL592435 Human DNA
c 594	14	70.0	134464	15	AP004114	AP004114 Oryza sat	c 667	14	70.0	161940	14	AC079289	AC079289 Homo sapi
c 595	14	70.0	134517	9	AC159229	AC159229 Mus muscu	c 668	14	70.0	161969	14	AC113571	AC113571 Canis fam
c 596	14	70.0	134963	8	HS1995U16	AL022151 Human DNA	c 669	14	70.0	162008	14	AC018792	AC018792 Homo sapi
c 597	14	70.0	135162	14	AC143100	AC143100 Macaca mu	c 670	14	70.0	162081	8	AC007542	AC007542 Homo sapi
c 598	14	70.0	136267	5	CR382334	CR382334 Zebrafish	c 671	14	70.0	162119	8	CNS05TEO	AL359237 Human chr
c 599	14	70.0	138665	14	AC020447	AC020447 Drosophil	c 672	14	70.0	162131	9	AC136456	AC136456 Mus muscu
c 600	14	70.0	138846	15	AC140850	AC140850 Medicago	c 673	14	70.0	162240	14	AC145756	AC145756 Pan trogl
c 601	14	70.0	138860	9	AL713956	AL713956 Mouse DNA	c 674	14	70.0	162265	8	AC018445	AC018445 Homo sapi
c 602	14	70.0	140468	14	AC017377	AC017377 Drosophil	c 675	14	70.0	162295	14	AC013768	AC013768 Homo sapi

676	14	70.0 162321	5	BX957244	14	70.0 179984	8	AC016526	AC016526 Homo sapi
677	14	70.0 162996	8	AC006441	14	70.0 180016	14	AC023090	AC023090 Homo sapi
c 678	14	70.0 163197	14	AC091392	14	70.0 180271	14	AC040913	AC040913 Homo sapi
c 679	14	70.0 163318	8	AC114772	14	70.0 180347	8	AC009415	AC009415 Homo sapi
c 680	14	70.0 163565	8	AL355339	14	70.0 181132	2	AC008206	AC008206 Drosophila
681	14	70.0 164179	14	AL445533	14	70.0 181322	15	CN8008C2	BN000512 Oryza sat
682	14	70.0 164272	8	AC073657	14	70.0 181442	2	AC114917	AC114917 Mus muscu
c 683	14	70.0 164369	14	AC158294	14	70.0 181480	2	AC009740	AC009740 Drosophila
c 684	14	70.0 164805	8	AC092940	14	70.0 181539	14	BX957351	BX957351 Danio rer
c 685	14	70.0 165164	8	AP002433	14	70.0 181835	8	AC146227	AC146227 Pan trogl
c 686	14	70.0 165196	9	AL596123	14	70.0 182241	8	AC022909	AC022909 Homo sapi
687	14	70.0 165255	14	AC021421	14	70.0 182261	14	AC162037	AC162037 Mus muscu
c 688	14	70.0 166031	14	CR354375	14	70.0 182423	8	AL126942	AC126942 Mus muscu
c 689	14	70.0 167248	9	AC023645	14	70.0 182955	8	AL445237	AL445237 Human DNA
c 690	14	70.0 166185	5	BX649507	14	70.0 184121	8	AC016706	AC016706 Homo sapi
691	14	70.0 166258	14	AL451066	14	70.0 184313	8	AL445584	AL445584 Human DNA
c 692	14	70.0 166287	8	AC026843	14	70.0 184864	8	AC018927	AC018927 Homo sapi
c 693	14	70.0 166797	8	AC124864	14	70.0 184875	8	AC025898	AC025898 Homo sapi
c 694	14	70.0 167122	14	AC053532	14	70.0 185462	14	AC074377	AC074377 Mus muscu
695	14	70.0 167248	9	AC102297	14	70.0 185673	14	AC141142	AC141142 Rattus no
c 696	14	70.0 167566	14	AC123426	14	70.0 186387	9	AC122885	AC122885 Mus muscu
c 697	14	70.0 168059	2	AC010027	14	70.0 185717	14	AC123396	AC123396 Rattus no
c 698	14	70.0 168158	9	AC139562	14	70.0 185825	2	AC091204	AC091204 Drosophila
c 699	14	70.0 168197	9	AC137511	14	70.0 185825	9	AL671868	AL671868 Mouse DNA
c 700	14	70.0 168559	8	AP003307	14	70.0 186052	8	AC104187	AC104187 Homo sapi
701	14	70.0 168566	15	AP005297	14	70.0 186087	9	AL645909	AL645909 Mouse DNA
702	14	70.0 168571	14	AC133273	14	70.0 186387	9	AC122885	AC122885 Mus muscu
c 703	14	70.0 168909	14	AC118862	14	70.0 186492	14	AC162617	AC162617 Bos tauru
c 704	14	70.0 169045	8	AC005544	14	70.0 186783	8	AC090355	AC090355 Homo sapi
705	14	70.0 169117	14	CR735127	14	70.0 187005	8	BX664735	BX664735 Human DNA
c 706	14	70.0 169313	8	AP001782	14	70.0 187167	14	AP001563	AP001563 Homo sapi
c 707	14	70.0 170324	2	AC007805	14	70.0 187252	9	AL607109	AL607109 Mouse DNA
c 708	14	70.0 170330	8	AC092896	14	70.0 187298	8	AC018691	AC018691 Homo sapi
709	14	70.0 170695	8	AC016134	14	70.0 188530	14	AC079547	AC079547 Mus muscu
710	14	70.0 170943	14	AC166591	14	70.0 188603	14	CR848710	CR848710 Danio rer
c 711	14	70.0 171193	14	AC118923	14	70.0 188643	8	AC142329	AC142329 Pan trogl
712	14	70.0 171428	8	AC013407	14	70.0 188735	9	AC111091	AC111091 Mus muscu
c 713	14	70.0 171621	14	AC011961	14	70.0 189104	14	AC161229	AC161229 Mus muscu
c 714	14	70.0 171754	8	CNS01DVG	14	70.0 189215	9	AC124490	AC124490 Mus muscu
715	14	70.0 171936	14	AC120031	14	70.0 189608	14	AC155612	AC155612 Zea mays
c 716	14	70.0 172090	14	AC051661	14	70.0 189711	5	CR318631	CR318631 Zebrafish
717	14	70.0 172286	9	AC119211	14	70.0 189763	9	AC109617	AC109617 Mus muscu
718	14	70.0 172367	14	AC118989	14	70.0 190631	9	AC124755	AC124755 Mus muscu
719	14	70.0 172390	2	AC008090	14	70.0 190681	8	AC073389	AC073389 Homo sapi
c 720	14	70.0 172453	14	AC015889	14	70.0 190755	9	AC120162	AC120162 Mus muscu
c 721	14	70.0 172984	8	AC063949	14	70.0 191072	14	CR854853	CR854853 Homo sapi
c 722	14	70.0 173126	8	AC005988	14	70.0 191279	9	AL672001	AL672001 Mouse DNA
723	14	70.0 173367	14	AC148147	14	70.0 191296	8	AC023949	AC023949 Homo sapi
724	14	70.0 173445	8	AC078876	14	70.0 191673	14	AL356743	AL356743 Homo sapi
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## ALIGNMENTS

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DEFINITION Sequence 12 from patent US 6777182.  
ACCESSION AR576665  
VERSION AR576665.1 GI:56578950  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 254)  
AUTHORS Baban,S., Bernard,M., Cherry,E., Gosselin,D., Hugo,P., Malette,B.,  
Miron,P., Prive,C. and Shazand,K.  
TITLE Methods for determining the likelihood of endometriosis in a female  
JOURNAL Subject  
Patent: US 6777182-A 12 17-AUG-2004;  
Metriogene Biosciences Inc.; Montreal;  
CAX;  
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Db 90 GCTTTGGTTGGGCAACACAT 71  
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DEFINITION Sequence 12 from Patent WO0162959.  
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VERSION AX229886.1 GI:15592021  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Baban,S., Bernard,M., Cherry,E., Gosselin,D., Hugo,P., Malette,B.,  
Miron,P., Prive,C. and Shazand,K.  
TITLE Endometriosis-related markers and uses thereof  
JOURNAL Patent: WO 0162959-A 12 30-AUG-2001;  
Procera Biosciences Inc. (CA)  
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VERSION CQ679217.1 GI:42191349  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.  
TITLE Compositions and methods relating to osteoarthritis  
JOURNAL Patent: WO 02070737-A 24143 12-SEP-2002;  
Chondrogene Inc. (CA)  
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ACCESSION CQ690723  
VERSION CQ690723.1 GI:42228057  
KEYWORDS Homo sapiens (human)  
SOURCE



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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Liaw,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 35649 12-SEP-2002;
Chondrogene Inc. (CA)
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Db 95 GCTTTGGTTGGGCAACACAT 76
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DEFINITION Sequence 201 from Patent WO03039443.
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VERSION AX778044.1 GI:32695038
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,
Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.
TITLE Novel genetic markers for leukemias
JOURNAL Patent: WO 03039443-A 201 15-MAY-2003;
Deutsches Krebsforschungszentrum (DE);
Ludwig-Maximilian-Universitaet Muenchen (DE); Haferlach, Torsten,
PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)
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DEFINITION Homo sapiens forkhead box O1A (rhabdomyosarcoma) mRNA, complete
cds.
ACCESSION BT007455
VERSION BT007455.1 GI:30583748
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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Hominidae; Homo.
1 (bases 1 to 1968)
Kalinine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
vector
Unpublished
2 (bases 1 to 1968)
Kalinine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Direct Submission
Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the SalI and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after SalI site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/orfclones.
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/lab_host="DH5alpha T1 resistant"
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7
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LOCUS AY890173 1968 bp mRNA linear SYN 29-MAR-2005
DEFINITION Synthetic construct Homo sapiens clone FLH015808.01X forkhead box
O1A (FOXO1A) mRNA, complete cds.
ACCESSION AY890173
VERSION AY890173.1 GI:61361857
KEYWORDS Human ORF Project.
SOURCE synthetic construct
ORGANISM synthetic construct

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REFERENCE	other sequences; artificial sequences.	synthetic construct
AUTHORS	1. (bases 1 to 1968)	synthetic construct
	Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and LaBaer, J.	other sequences; artificial sequences.
TITLE	Cloning of human full-length CDS in Creator (TM) recombinational vector system	1 (bases 1 to 1968)
JOURNAL	Unpublished	Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and LaBaer, J.
REFERENCE	2 (bases 1 to 1968)	Cloning of human full-length CDS in Creator (TM) recombinational vector system
AUTHORS	Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and LaBaer, J.	Unpublished
TITLE	Direct Submission	2 (bases 1 to 1968)
JOURNAL	Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA	Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and LaBaer, J.
COMMENT	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sali and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sali site and before 'ATG' to provide Kozak consensus sequence. Each clone is clonally isolated and full-length sequence-verified.	Direct Submission
FEATURES	Location/Qualifiers	Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
source	1. .1968	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sali and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sali site and before 'ATG' to provide Kozak consensus sequence. Each clone is clonally isolated and full-length sequence-verified.
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	/gene="FOXO1A"	/note="derived from MGC template"
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KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE  
AUTHORS Nakaie J., Park, B.C. and Accili, D.  
TITLE Insulin stimulates phosphorylation of the forkhead transcription factor FOXO on serine 253 through a Wortmannin-sensitive pathway  
JOURNAL J. Biol. Chem. 274 (23), 15982-15985 (1999)  
PUBMED 10347145  
REFERENCE  
AUTHORS Nakaie J. and Accili, D.  
TITLE Direct Submission  
JOURNAL Submitted (04-FEB-1999) Developmental Endocrinology Branch, National Institutes of Health, Building 10, Room 10D18, Bethesda, MD 20892, USA  
FEATURES  
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VERSION AY094061.1 GI:20384962  
KEYWORDS  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
REFERENCE  
AUTHORS Zhu, Q., Cunningham, M.A. and Hammond, J.M.  
TITLE FOXO Expression in Porcine Granulosa Cells  
JOURNAL Unpublished  
REFERENCE  
2 (bases 1 to 2162)

AUTHORS Zhu, Q., Cunningham, M.A. and Hammond, J.M.  
TITLE Direct Submission  
JOURNAL Submitted (02-APR-2002) Dept. of Medicine/Div. of Endocrinology, Pennsylvania State Univ. College of Medicine, 500 University Dr., Hershey, PA 17033, USA  
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DB 1973 GCTTTGGTTGGGCAACACAT 1954  
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DEFINITION Homo sapiens forkhead box O1a (rhabdomyosarcoma), mRNA (cDNA clone MGC:1750 IMAGE:2959021), complete cds.  
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VERSION BC021981.2 GI:33869892  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 2413)  
Klausner, R.D., Collins, P.S., Wagner, L., Sherman, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshikiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Rulyk, S.W., Villalón, D.C., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Buckerfield, Y.S., Krzywinbki, M.I., Skalska, U., Smalley, D.E.,

CONSRMT  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
CONSRMT  
TITLE  
JOURNAL  
REMARK  
COMMENT

Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
Mammalian Gene Collection Program Team  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 2413)

NIH MGC Project  
Direct Submission  
Submitted (22-JAN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
On Aug 19, 2003 this sequence version replaced gi:18314374.  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbioology.org>  
contact: [amadansystemsbioology.org](mailto:amadansystemsbioology.org)  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha  
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 2 Row: 0 Column: 10.

FEATURES  
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Location/Qualifiers  
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Query Match 100.0%; Score 20; DB 8; Length 2413;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCCTTGGTTGGCAACACAT 20  
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RESULT 12  
AF114258/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
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PUBMED  
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AUTHORS  
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JOURNAL  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 2294 GCCTTGGTTGGCAACACAT 2275

RESULT 13  
BC070065/c  
LOCUS  
DEFINITION

BC070065 2482 bp mRNA linear PRI 21-JUL-2005  
Homo sapiens forkhead box O1a (rhabdomyosarcoma), mRNA (cdna clone  
IMAGE:30345006), partial cds.

[illegible]

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ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 2503;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2311 GCTTTGGTTGGCAACACAT 2292

RESULT 15  
AF178854/c  
LOCUS  
DEFINITION Synthetic construct Pax3-forkhead fusion protein (Pax3/FKHR) mRNA,  
complete cds.  
ACCESSION AF178854  
VERSION AF178854.1 GI:6636096  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 2725)  
AUTHORS Lam, P.Y.P., Sublett, J.E., Hollenbach, A.D., Rousset, M.F.,  
Epstein, J.A., Song, B., Lakkis, M. and Wang, C.  
TITLE Author's Corrections  
JOURNAL Mol. Cell. Biol. (2000) In press  
AUTHORS Naeye, C.W., Rakestraw, K., Hollenbach, A.D., Grosfeld, G. and  
Rousset, M.F.  
TITLE Direct Submission  
JOURNAL Submitted (19-AUG-1999) Hartwell Center for Bioinformatics &  
Biotechnology, St. Jude Children's Research Hospital, 332 N.  
Lauderdale St., Memphis, TN 38105, USA

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Query Match 100.0%; Score 20; DB 11; Length 2725;  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2671 GCTTTGGTTGGCAACACAT 2652

RESULT 16  
HSU02368/c  
LOCUS  
DEFINITION Human Pax3/forkhead transcription factor gene fusion mRNA, complete  
cds.

ACCESSION U02368  
VERSION U02368.1 GI:431253  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1 (bases 1 to 3200)  
AUTHORS Shapiro, D.N., Sublett, J.E., Li, B., Downing, J.R. and Naeye, C.W.  
TITLE Fusion of Pax3 to a member of the forkhead family of transcription  
factors in human alveolar rhabdomyosarcoma

JOURNAL Cancer Res. 53 (21), 5108-5112 (1993)  
PUBMED 8221646  
REFERENCE 2 (bases 1 to 3200)  
AUTHORS Shapiro, D.N.  
TITLE Direct Submission  
JOURNAL Submitted (04-OCT-1993) Shapiro D.N., St. Jude Children's Research  
Hospital, Experimental Oncology, 332 North Lauderdale, Memphis, TN  
38105, USA

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 2511 GCTTTGGTTGGCAACACAT 2492  
RESULT 17  
CQ874011/c CQ874011 3421 bp DNA linear PAT 27-SEP-2004  
LOCUS Sequence 430 from Patent WO2004076622.  
DEFINITION CQ874011  
ACCESSION CQ874011  
VERSION CQ874011.1 GI:52747603  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Taira, K. and Kawasaki, H.  
TITLE Regulation of mammalian cells  
JOURNAL Patent: WO 2004076622-A 430 10-SEP-2004;  
National Institute of Advanced Industrial Science and Tec hnology  
(JP)  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTTTGGTTGGCAACACAT 20  
Db 1926 GCTTTGGTTGGCAACACAT 1907  
RESULT 18  
HSU02310/c HSU02310 3421 bp mRNA linear PRI 16-DEC-1993  
LOCUS

Human fork head domain protein (FKHR) mRNA, complete cds.  
U02310  
VERSION U02310.1 GI:435422  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3421)  
AUTHORS Galili, N.  
TITLE Fusion of a fork head domain to PAX-3 in the solid tumor alveolar  
rhabdomyosarcoma  
JOURNAL Nature Genetics 5(3), 230-235 (1993)  
REFERENCE 2 (bases 1 to 3421)  
AUTHORS Galili, N., Davis, R.J., Fredericks, W.J., Mukhopadhyay, S.,  
Rauscher, F.J. III, Emanuel, B.S., Rovera, G. and Barr, F.G.  
TITLE Direct Submission  
JOURNAL Submitted (01-OCT-1993) Naomi Galili, Wistar Institute, 3606 Spruce  
Street, Philadelphia, PA 19104 USA  
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Db 1926 GCTTTGGTTGGCAACACAT 1907  
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HSU02308/c HSU02308 3517 bp mRNA linear PRI 16-DEC-1993  
LOCUS Human PAX-3-FKHR gene fusion mRNA, partial cds.  
DEFINITION U02308  
ACCESSION U02308.1 GI:435418  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3517)  
AUTHORS Galili, N., Davis, R., Fredericks, W.J., Mukhopadhyay, S.,  
Rauscher, F.J. III, Emanuel, B.S., Rovera, G. and Barr, F.G.  
TITLE Fusion of a fork head domain gene to PAX3 in the solid tumor  
alveolar rhabdomyosarcoma

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JOURNAL Nature Genetics 5(3), 230-235 (1993)
REFERENCE 2 (bases 1 to 3517)
AUTHORS Galili,N.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1993) Naomi Galili, Wistar Institute, 3606 Spruce
Street, Philadelphia, PA 19104 USA
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Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20
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Db 2022 GCTTTGGTTGGCAACACAT 2003

RESULT 20
CQ724998/c 4714 bp DNA linear PAT 03-FEB-2004
LOCUS Sequence 10932 from Patent WO02068579.
DEFINITION CQ724998
ACCESSION CQ724998
VERSION CQ724998.1 GI:42285855
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
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    Hominidae; Homo.
REFERENCE 1
    Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
    Kits, such as nucleic acid arrays, comprising a majority of
    humanexons or transcripts, for detecting expression and other uses
    thereof
    Patent: WO 02068579-A 10932 06-SEP-2002;
    PE Corporation (NY) (US)
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RESULT 21
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LOCUS Homo sapiens mRNA; cDNA DKFZp686B20125 (from clone DKFZp686B20125).
DEFINITION BX648278
ACCESSION BX648278
VERSION BX648278.1 GI:34367437
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
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        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
    REFERENCE 1 (bases 1 to 4919)
        Bloecher,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Oeanger,A.,
        Fobo,G., Han,M. and Wiemann,S.
        The German Human cDNA Consortium
        Direct Submission
        Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
        Neuherberg, GERMANY
        Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
        Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
        sequenced by GBF (National Research Centre for Biotechnology Ltd.,
        Braunschweig/Germany) within the cDNA sequencing consortium of the
        German Genome Project.
        This clone (DKFZp686B20125) is available at the RZPD in Berlin.
        Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
        Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
        information about the clone and the sequencing project is available
        at http://mips.gsf.de/proj/cDNA/.
    FEATURES
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        Best Local Similarity 100.0%; Pred. No. 0.27;
        Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20
    |||||
Db 1508 GCTTTGGTTGGCAACACAT 1489

RESULT 22
MMU252157/c 4945 bp mRNA linear ROD 15-APR-2005
LOCUS Mus musculus mRNA for forkhead protein FKHR (FKhr gene).
DEFINITION MMU252157
ACCESSION AJ252157
VERSION AJ252157.1 GI:7530135
KEYWORDS FKhr gene; forkhead protein FKHR.
SOURCE Mus musculus (house mouse)
    ORGANISM Mus musculus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
        Sciurognathi; Muridae; Murinae; Mus.
    REFERENCE 1
        Leenders,H., Benoit,C. and Mathis,D.
        The forkhead FKHR is involved in thymocyte proliferation
        Unpublished
        JOURNAL
        REFERENCE 2 (bases 1 to 4945)
        Leenders,H.
        Direct Submission
        Submitted (06-JAN-2000) Leenders H., Alsace, IGBMC, BP 163, 67404
```

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FEATURES
    source
        Illkirch, C.U. de Strasbourg, 67404, FRANCE
        Location/Qualifiers
            1. .4945
                /organism="Mus musculus"
                /mol_type="mRNA"
                /db_xref="taxon:10090"
                /tissue_lib="P19 embryonal carcinoma phage library"
            1. .4945
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            1. .428
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            429. .2387
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            /codon_start=1
            /product="forkhead protein FKHR"
            /protein_id="CAB86873.1"
            /db_xref="GI:7530136"
            /db_xref="GOA:O9UJW4"
            /db_xref="InterPro:IPR001766"
            /db_xref="InterPro:IPR011991"
            /db_xref="MG1:I8990077"
            /db_xref="UniProt/Tx:EMBL:Q9UJW4"
            /translation="MAEAPQVETDPDFEPLPRQSCWTLPRPEFNQSNSTSSPAP
            SGGAAAPDAASLASASASTDPMNSLLESEDEFARAPGCVAAVAASARGCLG
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            SYADLTILAKSSAEKKLTLSQIYEWVVKSVYFQKQNSNSAGWKNKSNIRHLSLHS
            KFRIVQNEGTSGSSKMWMLNPEGGKSGKSPRRASMDNNSKFAKSGRGAACKCAKLSQ
            QGEGQDSGSGQFSKWPASQGSNDDFDNWSTFPRPTSSNASTISGRLSPTVTEQDD
            LGQDVSILVVPSSAAWASTLPSLSBISNPENNELLDNLILLSPSTLSVTSQSSP
            GSNMQQTPCYSPASPNSLANSPSNYKYTGQSSMSPLQPMQMTLQDSKSYGGLG
            QYNACPLLKELLTSDSPPHNDIMSVPDQVAQPSNRVLCQNYMGNSNWPAYGQGA
            SHKNMNPSSHTPHGAQQTASVNGRTPLPHVNTMPHTSAWNRLLTPVKTPQLQVPLSH
            MQMSLGSYSVSGNSCGNGRMGVLHQEKLPSLDLQGMFIERLDLDCDMESIIRNDLMDQD
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            2388. .4945
                /gene="Fkhr"
    3'UTR

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Query Match	100.0%;	Score 20;	DB 9;	Length 4945;	
Best Local Similarity	100.0%;	Pred. No. 0.27;			
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Qy	1	GCATTGGTTGGGCAACACAT	20		
Db	2339	GCATTGGTTGGGCAACACAT	2320		
RESULT 23					
CS031181/c					
LOCUS	CS031181	5723 bp	DNA	linear	PAT 10-MAR-2005
DEFINITION	Sequence 687 from Patent WO2005016962.				
ACCESSION	CS031181				
VERSION	CS031181.1	GI:60731351			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Abbas, A., Clark, H., Ouyang, W., Williams, M.P., Wood, W.I. and Wu, T.D.				
TITLE	Compositions and methods for the treatment of immune related diseases				
JOURNAL	Patent: WO 2005016962-A 687 24-FEB-2005;				
FEATURES	Genentech, Inc. (US)				
source	Location/Qualifiers				
	1. .5723				
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
ORIGIN					
Query Match	100.0%;	Score 20;	DB 6;	Length 5723;	

Best Local Similarity 100.0%; Pred. No. 0.27; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	2305	GCITTTGGTTGGCAACACAT	2286						
RESULT 24									
CS040133/c									PAT 22-MAR-2005
LOCUS	CS040133		5723 bp	DNA	linear				
DEFINITION	Sequence 687 from Patent WO2005019258.								
ACCESSION	CS040133								
VERSION	CS040133.1	GI:61847976							
KEYWORDS									
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	1								
AUTHORS	Abbas, A., Clark, H., Ouyang, W., Williams, P.M., Wood, W.I. and Wu, T.D.								
TITLE	Compositions and methods for the treatment of immune related diseases								
JOURNAL	Patent: WO 2005019258-A 687 03-MAR-2005;								
FEATURES	Genentech, Inc. (US)								
source	Location/Qualifiers								
	1..5723								
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	/db_xref="taxon:9606"								
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Query Match		100.0%;	Score 20;	DB 6;	Length 5723;				
Best Local Similarity		100.0%;	Pred. No. 0.27;						
Matches	20;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	GCTTTGGTTGGCAACACAT	20						
Db	2305	GCITTTGGTTGGCAACACAT	2286						
RESULT 25									
AX587664/c									PAT 10-JAN-2003
LOCUS	AX587664		5723 bp	DNA	linear				
DEFINITION	Sequence 134 from Patent WO0246467.								
ACCESSION	AX587664								
VERSION	AX587664.1	GI:28212364							
KEYWORDS									
SOURCE	synthetic construct								
ORGANISM	synthetic construct								
REFERENCE	1								
AUTHORS	Bertucci, F., Houlgatte, R., Birnbaum, D., Nguyen, C., Viens, P. and Fort, V.								
TITLE	Gene expression profiling of primary breast carcinomas using arrays of candidate genes								
JOURNAL	Patent: WO 0246467-A 134 13-JUN-2002;								
FEATURES	Ipsogen (FR)								
source	Location/Qualifiers								
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	/notes="forkhead box oia (rhbdomyoarcoma) (FOXO1A) gene."								
ORIGIN									
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Best Local Similarity		100.0%;	Pred. No. 0.27;						
Matches	20;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;



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Qy 1 GCTTTGGTTGGCAACACAT 20
Db 2305 GCTTTGGTTGGCAACACAT 2286

RESULT 26
AF032885/c
LOCUS AF032885 Homo sapiens forkhead protein (FKHR) mRNA, complete cds.
DEFINITION AF032885 Homo sapiens forkhead protein (FKHR) mRNA, complete cds.
ACCESSION AF032885
VERSION AF032885.1 GI:2895491
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 5723)
Anderson, M.J., Viars, C.S., Czekay, S., Cavenee, W.K. and Arden, K.C.
Cloning and characterization of three human forkhead genes that
comprise an FKHR-like gene subfamily
Genomics 47 (2), 187-199 (1998)
JOURNAL PUBMED 9479491
REFERENCE 2 (bases 1 to 5723)
Anderson, M.J., Viars, C.S., Czekay, S., Cavenee, W.K. and Arden, K.C.
Direct Submission
Submitted (03-NOV-1997) Medicine, Ludwig Institute for Cancer
Research, San Diego Branch, 9500 Gilman Drive, La Jolla, CA
92093-0660, USA
FEATURES
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Location/Qualifiers
1..5723
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="13"
.map="13q13-q14.1"
1..5723
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386..2353
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/codon_start=1
/product="forkhead protein"
/protein_id="AAC39591.1"
/db_xref="GI:2895492"
/translation="MARAPQVVEIDPDPEPLPRSCVWPLPRPEFSQNSATSSPAP
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GNLSYADLITKAIESSAEKRLTSLQIYEMVYKVPYFKDGDSSAGWKNISIRNLN
LHSEFIRVNEGTVGQKSWMLNPEGSGSGSPRRRAASMDNNKSPAKSRRAAKKAS
LQSQEGAGSPGSGKWPASPGSHNDPDFDNTSPRTSPRTSSNAFTSGRLSPIMTE
QDDLEGDVHSMVYPPSAKMAWTLPSLSEISNPNMENLNLNLSSPTSLTVSTQ
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GMSYCNAGPLKLLTSDSPPHNDIMTPVDGVAQNSRVLGQVWGNVSNVSTYG
SQASHNKNMPPSSHTFGHAQQTSAVNGRPLPHTVSTPMTSPHTSGMRLTQVKTQVQVPL
PHPMQALGYSVSSVSCNGYGRMGLLHQELKPSDLDCMFIERLDCMESIIRNDLMD
GDTLDFDNVLPNQSPHPSVKTTTTHSWVSG"

Qy 1 GCTTTGGTTGGCAACACAT 20
Db 2305 GCTTTGGTTGGCAACACAT 2286

RESULT 27
AX779990/c
LOCUS AX779990 Homo sapiens forkhead protein (FKHR) mRNA, complete cds.
DEFINITION AX779990 Sequence 2147 from Patent WO03039443.
ACCESSION AX779990
VERSION AX779990.1 GI:32696984

Qy 1 GCTTTGGTTGGCAACACAT 20
Db 2305 GCTTTGGTTGGCAACACAT 2286

RESULT 28
AL133318
LOCUS AL133318 81862 bp DNA linear PRI 18-MAY-2005
DEFINITION Human DNA sequence from clone RP11-89L15 on chromosome 13 Contains
the 3' end of the FOXO1A gene for forkhead box O1A
(rhabdomyosarcoma), complete sequence.
ACCESSION AL133318
VERSION AL133318.11 GI:13784997
KEYWORDS HTG; FOXO1A; rhabdomyosarcoma.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 81862)
Beasley, H.
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Apr 24, 2001 this sequence version replaced gi:13374937.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
RP11-89L15 is from the library RPC1-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk
-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
```



30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone, and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

#### FEATURES

##### Location/Qualifiers

1. 81862  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosomes="13"  
/clone="RP11-89L15"  
/clone\_lib="RPC1-11.1"  
100

##### misc\_feature

/note="Clone right end: RP11-350A18"

##### gene

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complement(42965..44316),complement(39120..42490))  
/gene="FOXO1A"

##### mRNA

join(complement(RP11-89L15.1-001"  
/locus\_tag="RP11-89L15.1-001"  
/locus\_tag="FOXO1A"  
/locus\_tag="RP11-89L15.1-001"  
/product="forkhead box O1A (rhabdomyosarcoma)"  
/note="match: ESTs: AA019811 AAL34749 AA653517 AA727282  
AA746346 AA856624 AA866177 A1003947 A1188507 A1418347  
A1475740 A15233901 A1699468 A1741811 A1934945 A1936621  
AV645563 AV646573 AW020440 AW028783 AW121569 AW300151  
AW316979 AW367874 AW467069 AW476550 AW593488 AW621146  
AW949943 AW950024 BB633141 BE669435 BE850923 BF434989  
BF467469 BF509757 BF732882 BF733004 BF957712 BI044120  
BI183684 BI233985 BI414157 BI824376 BI838883 BM453915  
BM475689 BM678665 BM703023 BQ006072 BQ186082 BQ230226  
W07895  
match: cDNAs: AF032885 AF114258 AF114261 AF126056 AF178854  
AF384029 AJ252517 AY040320 AY094061 BC021981 U02308 U02310  
U02368 U36922"  
complement(39120)  
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complement(39148..39153)  
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complement(42979..44316))  
/gene="FOXO1A"  
/locus\_tag="RP11-89L15.1-001"  
/standard\_names="OTTHUMP0000018301"  
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Q9W79 Q9WH5"  
/codon\_start=1  
/product="forkhead box O1A (rhabdomyosarcoma)"  
/protein\_id="CA116970.1"  
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##### polyA\_site

/locus\_tag="RP11-89L15.1-001"

##### polyA\_signal

complement(39148..39153)

##### CDS

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/db\_xref="GI:5957149"

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GNLSADITLITAEISSAKRLTLQIYEMVKSVPYFKDGDSSAGKNSRRNLS  
LHSFPIVQNGTSGVSWMLNPEGSKSPRRASMDNNKFAKRSRAAKKAS  
LQSGOEGADSPGQFSKWPASPGSHNDPNNSTFPRPTSSNASTISGRSLTPMTE  
ODDLGEGDVHSMVYPPSAKMAWTLPSLSEISNPMENLIDNLLSSPSTLTVSTO  
SSPCTMCOQCYSPAPNTSINSFSPNYKYTYGQSSMSPLPQMPITLODNKSSYG  
GMSQVNAKGLLKELLTSDSPPHNDITPVDGVAQPNRSVLGQNMVGPNSVMSYTG  
QASNCNKPMSSSHTHGHAQQTSAVNGRPLPVTWPTSHGMRNLQVKTVPQVPL  
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/locus\_tag="RP11-89L15.1-002"  
/product="forkhead box O1A (rhabdomyosarcoma)"  
/note="match: ESTs: AL475740.1"

##### gene

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##### mRNA

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/product="forkhead box O1A (rhabdomyosarcoma)"  
/note="match: ESTs: AL475740.1"

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81862  
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#### ORIGIN

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Matches 20; Conservative 0; Mismatches 0;  
QY 1 GCTTTGGTTGGCAACACAT 20  
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DB 43027 GCTTTGGTTGGCAACACAT 43046

#### RESULT 29

AC163092/c  
LOCUS  
DEFINITION Mus musculus chromosome 3 clone RP24-212F17 map 3, \*\*\* SEQUENCING  
IN PROGRESS \*\*\*, 4 unordered pieces.  
AC163092  
AC163092.3 GI:71044075  
HTG; HTGS PHASE1; HTGS FULLTOP; HTGS\_ACTIVEFIN.  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 149841)  
Birren,B., Nusbaum,C. and Lander,E.  
MUS musculus chromosome 3, clone RP24-212F17  
JOURNAL  
2 (bases 1 to 149841)  
REFERENCE  
1 (bases 1 to 149841)  
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,  
Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,  
Bloom,T., Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J.,  
Chapel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,  
DeRellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,  
Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D.,  
Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,  
Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,  
Johnson,R., Jones,C., Karatas,A., Kells,C., Landers,T.,  
Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,  
Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,  
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,  
Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,  
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,  
Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,  
Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,  
Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,  
Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,  
Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,  
Zimmer,A. and Zody,M.

#### TITLE

JOURNAL  
Submitted (04-JUN-2005) Broad Institute of MIT and Harvard, 320  
Charles Street, Cambridge, MA 02141, USA  
3 (Bases 1 to 149841)  
REFERENCE  
AUTHORS  
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,  
Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,  
Bloom,T., Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J.,  
Chapel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,  
DeRellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,  
Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D.,  
Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,  
Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,  
Johnson,R., Jones,C., Karatas,A., Kells,C., Landers,T.,  
Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,  
Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,  
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,  
Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,  
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,  
Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,  
Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,  
Seaman,S., Sever,P., Smith,C., Spencer,B., Stange-Thomann,N.,

Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,  
Topham,K., Travers,M., Vassiliev,H., Venkataranan,V.S., Viel,R.,  
Vo.A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,  
Zimmer,A. and Zody,M.

# Direct Submission

Submitted (21-JUL-2005) Broad Institute of MIT and Harvard, 320

Charles Street, Cambridge, MA 02141, USA

On Jul 21, 2005 this sequence version replaced gi:67003692.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Broad Institute of MIT and Harvard

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@broad.mit.edu

----- Project Information

Center project name: L32659

Center clone name: 212\_F\_17

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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 17312: contig of 17312 bp in length  
\* 17313 17412: gap of unknown length  
\* 17413 59435: contig of 42023 bp in length  
\* 59436 59535: gap of unknown length  
\* 59536 94648: contig of 35113 bp in length  
\* 94649 94748: gap of unknown length  
\* 94749 149841: contig of 55093 bp in length.

## FEATURES

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

/chromosome="3"

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/clone\_lib="RPCI-24 Male Mouse BAC"

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/estimated\_length=unknown

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/estimated\_length=unknown

## ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 149841;

Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20

Db 86068 GCTTTGGTTGGCAACACAT 86049

## RESULT 30

AC078964

LOCUS

AC078964 155595 bp DNA linear HTG 15-JAN-2001

DEFINITION Homo sapiens chromosome 8 clone RP11-135C3 map 8, WORKING DRAFT

SEQUENCE, 23 unordered pieces.

AC078964

AC078964.2 GI:12229296

VERSION HTG; HTGS PHASE1; HTGS\_DRAFT.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

## REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

Hominidae; Homo.

1 (bases 1 to 155595)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 8, Clone RP11-135C3

Unpublished

2 (bases 1 to 155595)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Barna,N., Bastien,V., Bida,P., Boguslavsky,L.,  
Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,  
Chapel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,  
Dereallano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,  
FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,  
Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,  
Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRoque,K.,  
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G.,  
Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,  
McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,  
Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,  
O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K.,  
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,  
Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,  
Sougnaz,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,  
Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo.A.,  
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,  
Zimmer,A. and Zody,M.

Direct Submission

Submitted (13-AUG-2000) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jan 15, 2001 this sequence version replaced gi:9799780.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L10496

Center clone name: 135\_C\_3

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 144191 bases at least Q40

Consensus quality: 150273 bases at least Q30

Consensus quality: 152425 bases at least Q20

Insert size: 160000; agarose-fp

Insert size: 153395; sum-of-contigs

Quality coverage: 3.8 in Q20 bases; agarose-fp

Quality coverage: 4.0 in Q20 bases; sum-of-contigs

-----

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 23 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* 1 1089: contig of 1089 bp in length

\* 1090 1189: gap of 100 bp

\* 1190 2528: contig of 1339 bp in length

\* 2529 2628: gap of 100 bp

\* 2629 5195: contig of 2567 bp in length

\* 5196 5295: gap of 100 bp

\* 5296 6629: contig of 1334 bp in length

\* 6630 6729: gap of 100 bp

\* 6730 8429: contig of 1700 bp in length

\* 8430 8529: gap of 100 bp

\* 8530 30093: contig of 21564 bp in length

\* 30094 30193: gap of 100 bp





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Best Local Similarity 100.0%; Pred. NO. 0.18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGGCACACAT 20
   |||||
Db 154550 GCTTTGGTTGGGCACACAT 154531

RESULT 32
AC098951/c
LOCUS
DEFINITION Rattus norvegicus clone CH230-173B15, WORKING DRAFT SEQUENCE, 5
unordered pieces.
ACCESSION AC098951
VERSION AC098951.5 GI:30581568
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muridae; Murinae; Rattus.
          1 (bases 1 to 228076)
Muzny,D,Marie., Metzker,M,Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Chen,Y., Chen,Z., Chu,J.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Y.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,

```

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Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
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Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
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Lorensuhewa,L., Loulsegad,H., Lorado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartine,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
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Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Parks,K.,
Nwaokemele,O., Okwodu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu.L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.B., Shen,H.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajls,D.,
Sneid,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steinle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Umani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,X., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 228076)
Worley,K.C.
Direct Submission
Submitted (07-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 228076)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23100953.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GIJG
Center clone name: CH230-173B15
----- Summary Statistics

```

Assembly program: Atlas 3.0;  
 Consensus quality: 221795 bases at least Q40  
 Consensus quality: 222829 bases at least Q30  
 Consensus quality: 223416 bases at least Q20  
 Estimated insert size: 239975; sum-of-contigs estimation  
 Quality coverage: 8x in Q20 bases; sum-of-contigs estimation  
 -----  
 \* NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 5 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 220328: contig of 220328 bp in length  
 \* 220329 220428: gap of unknown length  
 \* 220429 224044: contig of 3616 bp in length  
 \* 224045 224144: gap of unknown length  
 \* 224145 225720: contig of 1576 bp in length  
 \* 225721 225820: gap of unknown length  
 \* 225821 226935: contig of 1115 bp in length  
 \* 226936 227035: gap of unknown length  
 \* 227036 228076: contig of 1041 bp in length.

#### FEATURES

Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10116"  
 /clone="CH230-173E15"

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 /note="wgs\_end\_extension  
 clone\_end:T7"

#### misc\_feature

137150..203514  
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 clone\_end:T7"

#### misc\_feature

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#### ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 228076;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GCTTTGGTTGGCAACACAT 20  
 |||||  
 Db 111636 GCTTTGGTTGGCAACACAT 111617

#### RESULT 33

AC113811/c

LOCUS

AC113811 303046 bp DNA linear HTG 20-NOV-2002

DEFINITION

Rattus norvegicus clone CH230-216D16, \*\*\* SEQUENCING IN PROGRESS

\*\*\*, 4 unordered pieces.

ACCESSION

AC113811

VERSION

AC113811.6 GI:25138632

KEYWORDS

HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.

SOURCE

Rattus norvegicus (Norway rat)

#### ORGANISM

Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

#### REFERENCE

1 (bases 1 to 303046)  
 Muzny,D,Marie., Metzker,M, Lee., Abramzon,S., Adams,C., Alder,J.,  
 Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,  
 Anyalebechi,V., Ayoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,  
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 Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,  
 Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,  
 Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,  
 Devila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,  
 Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,  
 Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,  
 Egan,A., Escotto,M., Eugene,C., Evans,C.A., Fall,T., Fan,G.,  
 Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,  
 Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,  
 Gabregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W.,  
 Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,  
 Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,  
 Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,  
 Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,  
 Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,  
 Karpthy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,  
 Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,  
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 Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,  
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 Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,  
 Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,  
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 Sanders,W., Savary,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,  
 Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajd,D.,  
 Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,  
 Steinle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,  
 Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,  
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 Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D. von  
 Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,  
 Weinatock,G. and Gibbs,R.A.

#### TITLE

Direct Submission

Unpublished

2 (bases 1 to 303046)

Worley,K.C.

Direct Submission

Submitted (05-MAR-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 303046)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:23195088.

The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas

(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described

in the feature table below represents a scaffold in the Atlas

assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GSHZ  
Center clone name: CH230-216D16  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 238069 bases at least Q40  
Consensus quality: 241686 bases at least Q30  
Consensus quality: 243440 bases at least Q20  
Estimated insert size: 246925; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 95547: contig of 95547 bp in length  
\* 95548 95647: gap of unknown length  
\* 95648 295240: contig of 199593 bp in length  
\* 295241 295340: gap of unknown length  
\* 295341 296872: contig of 1532 bp in length  
\* 296873 296972: gap of unknown length  
\* 296973 303046: contig of 6074 bp in length.

FEATURES  
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/note="wgs contig"

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misc\_feature

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misc\_feature

289420..291216  
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/estimated\_length=unknown

gap

296873..296972  
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ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 303046;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAACACAT 20

|||||

Db 75187 GCTTTGGTTGGCAACACAT 75168

RESULT 34

AE016828.11/c  
WFCOMMENT

Sequence split into 20 fragments LOCUS AE016828 Accession AE016828

Fragment Name Begin End  
AE016828\_00 1 110000  
AE016828\_01 100001 210000  
AE016828\_02 200001 310000  
AE016828\_03 300001 410000  
AE016828\_04 400001 510000  
AE016828\_05 500001 610000  
AE016828\_06 600001 710000  
AE016828\_07 700001 810000  
AE016828\_08 800001 910000  
AE016828\_09 900001 1010000  
AE016828\_10 1000001 1110000  
AE016828\_11 1100001 1210000  
AE016828\_12 1200001 1310000  
AE016828\_13 1300001 1410000  
AE016828\_14 1400001 1510000  
AE016828\_15 1500001 1610000  
AE016828\_16 1600001 1710000  
AE016828\_17 1700001 1810000  
AE016828\_18 1800001 1910000  
AE016828\_19 1900001 1995281

Continuation (12 of 20) of AE016828 from base 1100001 (AE016828 Cxiella burnetii RSA 49

Query Match 95.0%; Score 19; DB 1; Length 110000;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAACACA 19

|||||

Db 66215 GCTTTGGTTGGCAACACA 66197

RESULT 35

AJ834861

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AJ834861 Arabidopsis thaliana T-DNA flanking sequence, left border, clone 074G04.  
299 bp DNA linear PLN 22-SEP-2004

left border; T-DNA flanking sequence.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae;

Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurooids II; Brassicales; Brassicaceae; Arabidopsi.

1

Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,

Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,

Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences

of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)

12446565

2 (bases 1 to 299)

Balzergue, S.

Direct Submission

Submitted (21-SEP-2004) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment (s) resulting from

the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

<http://dbgap.versailles.inra.fr/publiclines/>. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplante' (<http://www.genoplante.com> and

<http://genoplante-info.infobiogen.fr>).

Location/Qualifiers







VMADLPTRPAAPFOFTTVDLFGPYLVKDVKREVTLTWGVFSCWACRAIHLDL  
VNSVSESLMAYQRTAIRGHPKSLMSPDPTNFGAKPVLQDLQFLESQNKALAE  
YAVSGTEWRQIHPDRGSHRGAAGAAVRAKRALQALDKMLTMSYSFQVLTAA  
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6418

variation

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/note="results in premature stop in Fugu Sequencing  
Project Scaffold M004397"  
/replaces="t"  
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/note="polypurine tract"  
6892. .7613  
/note="3' LTR"  
7614. .7618  
/note="integration site duplication"  
/rpt\_type=direct

ORIGIN

Query Match 85.0%; Score 17; DB 5; Length 7618;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 TTTGGTTGGCAACACA 19  
Db 4168 TTTGGTTGGCAACACA 4152

RESULT 38

FRIGVHL 40406 bp DNA linear VFR 13-JUN-2000  
LOCUS Fugu rubripes immunoglobulin heavy chain gene cluster, partial  
DEFINITION sequence.  
ACCESSION AF108421  
VERSION AF108421.1 GI:4633112  
KEYWORDS  
SEGMENT  
SOURCE  
ORGANISM  
Takifugu rubripes  
Takifugu rubripes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodontidae; Takifugu.  
1 (bases 1 to 40406)  
Peixoto, B.R. and Brenner, S.  
Characterization of approximately 50 kb of the immunoglobulin VH  
locus of the Japanese pufferfish, Fugu rubripes  
Immunogenetics 51 (6), 443-451 (2000)  
10866111  
2 (bases 1 to 40406)  
Peixoto, B.R. and Brenner, S.  
Direct Submission  
TITLE  
Submitted (23-NOV-1998) The Molecular Sciences Institute, 2168  
Shattuck Ave. 2nd Floor, Berkeley, CA 94704, USA  
FEATURES  
Location/Qualifiers  
1. .40406  
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/mol\_type="genomic DNA"  
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misc\_feature  
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18282. .22726  
/note="putative retrotransposon"  
Join(24516. .24555,24645. .24937)  
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V\_segment  
V\_segment  
V\_segment  
CDS

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ORIGIN

Query Match 85.0%; Score 17; DB 5; Length 40406;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 TTTGGTTGGCAACACA 19  
Db 35772 TTTGGTTGGCAACACA 35788

RESULT 39

AB024035/c  
LOCUS AB024035 78423 bp DNA linear PLN 14-FEB-2004  
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MHM17.  
ACCESSION AB024035 BA000015  
VERSION AB024035.1 GI:4519194  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
1  
Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E., Kotani, H.  
and Tabata, S.  
Structural analysis of Arabidopsis thaliana chromosome 5. X.  
Sequence features of the regions of 3,076,755 bp covered by sixty  
Pl and TAC clones

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

DNA Res. 7 (1), 31-63 (2000)  
10718197  
2 (bases 1 to 78423)  
Nakamura.Y.  
Direct Submission  
Submitted (24-FEB-1999) Yasukazu Nakamura, Kazusa DNA Research  
Institute, Department of Plant Gene Research; 1532-3, Yana,  
Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamura@kazusa.or.jp,  
Tel:81-438-52-3935, Fax:81-438-52-3934)  
Address for correspondence: kaos@kazusa.or.jp  
For the latest information on annotation of this clone, please see  
http://www.kazusa.or.jp/kaos/cgi-bin/agd\_graph.cgi?c=MHM17  
Genes with similarity to proteins in the databases are described in  
'product' or 'note' qualifiers. Genes that have no significant  
protein similarity are described as 'unknown protein'.  
The software programs used to predict genes include: Grail  
(Informatics Group, Oak Ridge National Laboratory,  
http://compbio.ornl.gov/Grail-1.3/),  
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),  
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of  
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and  
SplicePredictor (Volker Brendel, Stanford University,  
http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).  
Genes encoding tRNAs are predicted by tRNAscan-SG  
(Sean Eddy, Washington University School of Medicine, St. Louis,  
http://genome.wustl.edu/eddy/tRNAscan-SG/).  
This sequence may not be the entire insert of this clone. It may be  
shorter because we remove overlaps between neighboring submissions.  
The 5' clone is MP110 and the 3' clone is MUL3.  
Location/Qualifiers  
1. .78423  
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/ecotype="Columbia"  
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containing similarity to protein kinase  
gene\_id:MP110.5"  
/number=1  
/evidence=not experimental  
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CDS

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LYRSGL"  
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17919..18006,18095..18156,18245..18429,18562..18739,  
18827..18870,19017..19218,19684..19770)  
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/db\_xref="GI:8777435"  
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CKIEEPKGLKFEFFPDQYFKNTLLTKAYHIMDEDEPLEKAIQTEIDWYPGKCLTQ  
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CDS

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LYRSGL"  
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join(17089..17134,17217..17260,17389..17484,17694..17786,  
17919..18006,18095..18156,18245..18429,18562..18739,  
18827..18870,19017..19218,19684..19770)  
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ENUTPKRRVRVRLIQGHDEITKFRERALEAKYQKQLPYIKRYEIVNGAT  
EVEGAPEDAKDQDDEKTAEEKGVFWLTKNNDVISEBITERDEGALILYKDIKW  
CKIEEPKGLKFEFFPDQYFKNTLLTKAYHIMDEDEPLEKAIQTEIDWYPGKCLTQ  
KILKPKPKGAKNAKTIKTCECFSPFNFPQVDDDDIDDEERAELQNLMEQDY  
DIGSTIREKIIPIHAFWSFTGEALGEFEFIDDDDDIDDEDEDEDEDEDEDE  
DEEEYSKTKKFEIILQGGRPQVTDQOGERPPECKQ"  
complement (join(23174..23239,23666..24049,24174..24863,  
25283..25388,25491..25645))  
/note="unannotated protein product; gb|AAC78547.1  
gene\_id:MHM17.7  
similar to unknown protein"  
/codon\_start=1  
/evidence=not experimental  
/protein\_id="BAA97026.1"  
/db\_xref="GI:8777436"

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/translation="MMHILSCSYLISMDGYNEASERPSSSSSSGSLARSLFHEVRO
SVPLQNGHVPMSAFMNLPTVEIRPQESQRLAFNDTQRLFYQMKIEASLRWFPEDF
NRKSPANSDIYRPHYPSSSSSSPNNISLPLPLPKPSTTTTAVNVPVLPFP
LAPINMIHQHPEPLFRNQRREEMTQAILAVLTGPSPSPSTSSPQKGRATAPKR
YYTMSIDRGAFLPVRKOSMMTRAMSFTYRLNINQRFRTENATTHGEGSGGGG
GRYTSQATQOHMISERKREKLNESFOALRSLLPGTKKOKASVLSIAREQLSSL
QGEISKLLERNREAKLAGREIENDLRPERFNRIRHIPESRRTDLDRLVRL
GDIIRVDLMIHLLPLKQINNVLVSIEARTLAREAGDTSIVIVISLRLKEGEWDE
SAFQZAMRVVADLAH"
CDS
complement(join(29415..29718,29813..30081,30183..30443,
30529..30656,32107..32716))
/note="gene_id:MHM17.8"
/codon_start=1
/evidence=not experimental
/product="cytokinin oxidase"
/protein_id="BAA97027.1"
/db_xref="GI:8777437"
/translation="WASYNLRQSVRLAIITVIIITLSPITNTSPQWNILSHNEF
AGKLTSSSSVESATDFGHVTKIPSAVLIPSSVEDITDLKLSFDSQLSPLAARG
HGHSHRGQASADGVVNMRSVMNRDGIKVSRTCLYVDVDAWLMIEVLNKLLELGL
TPVSHDILYLTGVGTLSNGISGQTFRGPQITNVLEMDVITGGEIATCSKWNSD
LFFAVIGLGGQGIITRARIKLEVAPKAKMLRFLYIDFSEFRQERVIKTDGVDF
LEGSTMVHGPDPNVRSTYPPSDHLRIASVMKRVHVIYCLEVVKYDETQYVNEE
MEELSDSLNHRVGFYKDYVMDFLNRVTGELNKLKGQWDVPHPLNLFVPTQOI
SKFDGVFKGIIRNNITSGPVLVPMNRKNWDRMSAIPEDDVFYAVGLFSAGFD
NWEAFQENMEILKECEDANMGVIOYLPVHSSQEGWVRHFGFRWNIIFVRYKYKDPKM
ILSPQNIQFKINSS"
trna
complement(39239..39315)
/product="tRNA-Val"
/note="codon recognized: GUG; gene_id:MHM17.9"
/evidence=not experimental
complement(join(41045..41748,41932..42184))
/note="unnamed protein product; gene_id:MHM17.10
pir||T04268
/codon_start=1
/evidence=not experimental
/protein_id="BAA97028.2"

Query Match      85.0%; Score 17; DB 15; Length 78423;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACA 17
Db 70517 GCTTTGGTTGGCAACA 70501

RESULT 40
CP000084_08/c
WPCOMMENT
Sequence split into 13 fragments LOCUS CP000084 Accession CP000084
Fragment Name      Begin      End
CP000084_00        1      110000
CP000084_01       100001    210000
CP000084_02       200001    310000
CP000084_03       300001    410000
CP000084_04       400001    510000
CP000084_05       500001    610000
CP000084_06       600001    710000
CP000084_07       700001    810000
CP000084_08       800001    910000
CP000084_09       900001   1010000
CP000084_10      1000001   1110000
CP000084_11      1100001   1210000
CP000084_12      1200001   1308759
Continuation (9 of 13) of CP000084 from base 800001 (CP000084 Candidatus Pelagibacter ub

Query Match      85.0%; Score 17; DB 1; Length 110000;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACA 17
```

```
Db 94372 GCTTTGGTTGGCAACA 94356
|||||
RESULT 41
AV144116/c
LOCUS
DEFINITION
AV144116
AV144116.1 GI:27550042
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
1 (bases 1 to 47740)
Waterfield,N.R., Daborn,P.J. and ffrench-Constant,R.H.
Genomic islands in Photorhabdus
Trends Microbiol. 10 (12), 541-545 (2002)
12564983
2 (bases 1 to 47740)
Waterfield,N.R. and ffrench-Constant,R.H.
Direct Submission
Submitted (22-AUG-2002) Biology and Biochemistry, University of
Bath, Claverton Down, Bath BA2 7AY, UK
Location/Qualifiers
1..47740
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="Wt4"
/db_xref="taxon:29488"
<1..41116
misc_feature
/note="type III secretion system; pathogenicity island"
complement(<1..113)
CDS
/note="similar to acetate CoA-transferase, beta subunit
(atoA)"
/codon_start=1
/transl_table=1
/product="unknown"
/protein_id="AAO18069.1"
/db_xref="GI:27550086"
/transl_table="MNAQGVIAHRAALELQDGVNVLIGIPTQVNVLPD"
complement(116..775)
CDS
/note="similar to acetoacetyl-CoA transferase alpha
subunit"
/codon_start=1
/transl_table=1
/product="unknown"
/protein_id="AAO18070.1"
/db_xref="GI:27550087"
/transl_table="MKNKLISTQQAHEHYDGMTIMAGGFMGVGTPPHLITALLNSGV
KDLTIANDTAGIDVIGPLVNNRVKKVITSHGTNPETGRKMLAGEIEVLEVLPGT
LIERIRCGAGLGGFLPTGTVGVVBEGKQKITVNGDYLLELPLRADLALIQHLAD
YHGNLTQLSARNFNPVIALAADITLAEPRKLEVEVETPCVITPGALIDYIVYPRG
N"
complement(765..1046)
CDS
/note="similar to response regulator of ato, ornithine
decarboxylase antizyme (sensor ATOS), atoC"
/codon_start=1
/transl_table=1
/product="unknown"
/protein_id="AAO18071.1"
/db_xref="GI:27550088"
/transl_table="MKQEVNQRHPRASSDNYGWDRLTNSPKQMALCCDTVKVGMPLT
LQAKLYRLNHLPLSGRSEDIALLAYSLPYGHSPMNSIYIGNQVEK"
complement(1269..2351)
CDS
/note="similar to hemolysin from Fusobacterium nucleatum
clinical isolate found in GenBank Accession Number
AF525507"
/codon_start=1
/transl_table=1
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/product="unknown"  
/protein\_id="AAO18072.1"  
/db\_xref="GI:27550089"  
/translation="MSEKFIWVPEDQSYGHQSQTITPSSSPDKNIGFTFKMDAGE  
NTLTLNDNTNSIKAHDIHPRPSPVELKEQYIVHKAENTDKLGETINISGNLI  
ISGQKXPVPHLSQITDRIYIKLQNSSTLAIKANTVRI SGPKNKTLKPEESAVAI  
SGLSHLTVAEASVEIQEENVIKGNISLECD SITESKAMKLSHLVNIYNSNITLQDN  
AQLISSLINRITDLOBOGQPLFTVNTPLKAGATLLNLSNPGTDPPLDIHREDYDK  
GVFNFMAGKENTGVVIDVAPKANAYGLNTMLRKNFIAINGAVVETGDMQKYPDFS  
YKGRDNDNQVGTIIISLNPHLKS"  
3583..4038  
/note="hypothetical Orf"  
/codon\_start=1  
/evidence=not experimental  
/transl\_table=11  
/product="unknown"  
/protein\_id="AAO18073.1"  
/db\_xref="GI:27550090"  
/translation="MIEKTERIAELEKIIDSQLTSSIIYSVSNFVGNDDNHLTGGSILT  
RTYIMPMTVMGIVASVPIIGPNTDIKI KPLDFHVMTKYWNVGKILWLFQEARAIN  
GVIKYCVGDNFNVLASRAOGNNGSGSKNLKVVCVPGDLNTAQMLY"  
complement(4645..5766)  
/note="hypothetical Orf"  
/codon\_start=1  
/evidence=not experimental  
/transl\_table=11  
/product="unknown"  
/protein\_id="AAO18074.1"  
/db\_xref="GI:27550091"  
/translation="MFNYKNIHPYEGLKMTVFEPWPNNSQVYTKDYGTGSIILST  
QDSDFGLKGANFMAESETLTLQNDSDNIPIYFPFNNDGTDSKGGLDINVS  
AGTLIVYRLANDQNHVTDRSHTVAYLGCSANFILKNSGSLSKNPGTFWFMFDYV  
SNKPKILMNSNREFIKQTKI EDDVPARIFLASELSLESSKLTRESNLYLDGN  
FNYCNISIQKSTVTLNNGIMQKNDIEKNKTFKLAGSPLNLESFDGINFLPYLD  
NVYTPGELFNITTEGNEGKIMIEFSQGNPNKNINKIPDKGLIAINNKIIKKEK  
HEDYFTGYKPDQKNDHKFMIITISLKQDQYQSYQYVNV"  
6595..6900  
/note="similar to Erwinia chrysanthemi protease inhibitor  
inh"  
/codon\_start=1  
/transl\_table=11  
/product="unknown"  
/protein\_id="AAO18075.1"  
/db\_xref="GI:27550092"  
/translation="MKKFMGLVLLGIASANAGADKSLTLDQECIAQWYMSAS  
QSCDLSIWLKNDTCAITACRAVHFVVENGRFFPYQSVQIANCGGLKTDGC"  
8293..8508  
/note="similar to Yersinia enterocolitica major cold shock  
protein CspA2"  
/codon\_start=1  
/transl\_table=11  
/product="unknown"  
/protein\_id="AAO18076.1"  
/db\_xref="GI:27550093"  
/translation="MSNAMTGSVKWFNNDKGFGFISPKDGSKDVFHYSAIQSNFXT  
LEEGQVYSPFSIENGAKGPSAVNVIVLS"  
complement(8731..9123)  
/note="similar to YopT chaperone SycT from Yersinia  
enterocolitica"  
/codon\_start=1  
/transl\_table=11  
/product="unknown"  
/protein\_id="AAO18077.1"  
/db\_xref="GI:27550094"  
/translation="WTHDYHQLIHALPSKLGVPASSSTDNIYTLVDGRFOVLIGCVH  
DNWLQFLCELGAELSHANNLFGQWPAHVQGDLDGQTLWSQRPLAEVDVAELQAWLE  
RFIDDIQRLTPTNTQOPKXLPPLPSMRV"  
complement(9120..10055)  
/note="similar to YopT from Yersinia enterocolitica"  
/codon\_start=1  
/transl\_table=11  
/product="putative type III secreted effector LopT"  
/protein\_id="AAO18078.1"

/db\_xref="GI:27550095"  
/translation="MSPISGINHORIFPTQOLDTTAVNQPOGELSGKSLKVSSPRPGL  
LERLSATQNLPHCSMLDRQLTDDGKNQESSEFSFMIKDRIVHFAVSTKLGSVRDS  
ASKHGVBVTFKACTKGAFLDQIMKHQDTSGGVCESSAHWISAHAGESVFNQLYVG  
QKQGFHIDSLVSIKQMDQDPYAEQSI TSWMLRENGIQPSPLEVSGETSGKGT  
KDLNALIDTDGKSGYKISFGQWAGHTVAAAYVDQKGVTFPDPNFGEFSPDKTS  
FSWNFSQDPFWSKMYNKEIGLQNFVYSNPEKTR"  
complement(10231..10848)  
/note="similar to Pseudomonas aeruginosa PscL type III  
export protein"  
/codon\_start=1  
/transl\_table=11  
/product="LscL"  
/protein\_id="AAO18079.1"  
/db\_xref="GI:27550096"  
/translation="MLPFIKITTEHLQAPELQILRKADYQTCLSAQSLLDAARIQAG  
EIERDAQVEYQKELGAGIDAARAEQANXIHQTLQCCQYRQVEQQMSNVLQA  
VRKILKNYDVSLLTQIVREALSLVSNQKQVILRVNPEQATVREQISRHKDFPEIG  
YLEITADERLDQGCILETEVGIIDASLDSQLEAVMSAINNQMN"  
complement(10827..11453)  
/gene="lscK"  
/complement(10827..11453)  
/gene="lscK"  
/note="similar to Pseudomonas aeruginosa PscK type III  
export protein; similar to Pseudomonas aeruginosa PscK  
type III export protein"  
/codon\_start=1  
/transl\_table=11  
/product="LscK"  
/protein\_id="AAO18026.1"  
/db\_xref="GI:27550043"  
/translation="MATVLTPOYFRFCPSYIHSDDLPSBWLAVLSLPEWRNSPRLN  
GLLTPDLANDVDYELPTGLGNLALLQSCLEQLLTLGALLHGOAIRHCLLATSLRLH  
LDSLGEKPFCLKYFDIILIGNWPTQWRSILPAINVNYRFTSLQFLWTAMEPLSID  
FARKLSURLPPYENLAAPVPSQAEPLAQLACLKLAQVNTCYHLLK"  
complement(11454..12191)  
/gene="lscJ"  
/complement(11454..12191)  
/gene="lscJ"  
/note="similar to Pseudomonas aeruginosa PscJ type III  
export protein"  
/codon\_start=1  
/transl\_table=11  
/product="LscJ"  
/protein\_id="AAO18027.1"  
/db\_xref="GI:27550044"  
/translation="MKKPYIICVMLAVMLTGTCKIELYTGVSQKEGNEMLALLREAGI  
SSDKPDKDNIGIKLLVEEDVAQAVEYLRKRGYPRENFSLLQDVFPKGLTSSPIER  
ARLNFAKAQEIARTLSIEDGLVARVHVVLPEEQDKLGKGLSPASSSVFIKHAADVQ  
DTYIPOIKOLVNNSEIGLSYDRISVVLVPAAGVRQVPLAPRYSTLFSIQVTEESQGR  
IGLLVLLALLFVSNLAQFLMHSRMQ"  
complement(12198..12536)  
/gene="lscI"  
/complement(12198..12536)  
/gene="lscI"  
/note="similar to Pseudomonas aeruginosa PscI type III  
export protein"  
/codon\_start=1  
/transl\_table=11  
/product="LscI"

Query Match 80.0%; Score 16; DB 1; Length 47740;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 CTTTGGTTGGGCAACA 17  
|||||  
Db 30085 CTTTGGTTGGGCAACA 30070  
  
RESULT 42  
AC095920\_09/c  
WCOMMENT

Sequence split into 10 fragments LOCUS AC095920 Accession AC095920

Fragment Name	Begin	End
AC095920_00	1	110000
AC095920_01	100001	210000
AC095920_02	200001	310000
AC095920_03	300001	410000
AC095920_04	400001	510000
AC095920_05	500001	610000
AC095920_06	600001	710000
AC095920_07	700001	810000
AC095920_08	800001	910000
AC095920_09	900001	1005083

Continuation (10 of 10) of AC095920 from base 900001 (AC095920 Rattus norvegicus clone C

Query Match 80.0%; Score 16; DB 14; Length 105083;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAACACAT 20

|||||||

Db 49873 TGGTTGGGCAACACAT 49858

RESULT 43

AP008214\_026

WPCOMMENT

Sequence split into 285 fragments LOCUS AP008214 Accession AP008214

Fragment Name	Begin	End
AP008214_000	1	110000
AP008214_001	100001	210000
AP008214_002	200001	310000
AP008214_003	300001	410000
AP008214_004	400001	510000
AP008214_005	500001	610000
AP008214_006	600001	710000
AP008214_007	700001	810000
AP008214_008	800001	910000
AP008214_009	900001	1010000
AP008214_010	1000001	1110000
AP008214_011	1100001	1210000
AP008214_012	1200001	1310000
AP008214_013	1300001	1410000
AP008214_014	1400001	1510000
AP008214_015	1500001	1610000
AP008214_016	1600001	1710000
AP008214_017	1700001	1810000
AP008214_018	1800001	1910000
AP008214_019	1900001	2010000
AP008214_020	2000001	2110000
AP008214_021	2100001	2210000
AP008214_022	2200001	2310000
AP008214_023	2300001	2410000
AP008214_024	2400001	2510000
AP008214_025	2500001	2610000
AP008214_026	2600001	2710000
AP008214_027	2700001	2810000
AP008214_028	2800001	2910000
AP008214_029	2900001	3010000
AP008214_030	3000001	3110000
AP008214_031	3100001	3210000
AP008214_032	3200001	3310000
AP008214_033	3300001	3410000
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AP008214_035	3500001	3610000
AP008214_036	3600001	3710000
AP008214_037	3700001	3810000
AP008214_038	3800001	3910000
AP008214_039	3900001	4010000
AP008214_040	4000001	4110000
AP008214_041	4100001	4210000
AP008214_042	4200001	4310000
AP008214_043	4300001	4410000
AP008214_044	4400001	4510000

AP008214_045	4500001	4610000
AP008214_046	4600001	4710000
AP008214_047	4700001	4810000
AP008214_048	4800001	4910000
AP008214_049	4900001	5010000
AP008214_050	5000001	5110000
AP008214_051	5100001	5210000
AP008214_052	5200001	5310000
AP008214_053	5300001	5410000
AP008214_054	5400001	5510000
AP008214_055	5500001	5610000
AP008214_056	5600001	5710000
AP008214_057	5700001	5810000
AP008214_058	5800001	5910000
AP008214_059	5900001	6010000
AP008214_060	6000001	6110000
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AP008214_062	6200001	6310000
AP008214_063	6300001	6410000
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AP008214_065	6500001	6610000
AP008214_066	6600001	6710000
AP008214_067	6700001	6810000
AP008214_068	6800001	6910000
AP008214_069	6900001	7010000
AP008214_070	7000001	7110000
AP008214_071	7100001	7210000
AP008214_072	7200001	7310000
AP008214_073	7300001	7410000
AP008214_074	7400001	7510000
AP008214_075	7500001	7610000
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AP008214_078	7800001	7910000
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AP008214_086	8600001	8710000
AP008214_087	8700001	8810000
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AP008214_090	9000001	9110000
AP008214_091	9100001	9210000
AP008214_092	9200001	9310000
AP008214_093	9300001	9410000
AP008214_094	9400001	9510000
AP008214_095	9500001	9610000
AP008214_096	9600001	9710000
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AP008214_099	9900001	10010000
AP008214_100	10000001	10110000
AP008214_101	10100001	10210000
AP008214_102	10200001	10310000
AP008214_103	10300001	10410000
AP008214_104	10400001	10510000
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AP008214_106	10600001	10710000
AP008214_107	10700001	10810000
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AP008214_114	11400001	11510000
AP008214_115	11500001	11610000
AP008214_116	11600001	11710000
AP008214_117	11700001	11810000

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AP008214_118 11800001 11910000
AP008214_119 11900001 12010000
AP008214_120 12000001 12110000
AP008214_121 12100001 12210000
AP008214_122 12200001 12310000
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AP008214_186 18600001 18710000
AP008214_187 18700001 18810000
AP008214_188 18800001 18910000
AP008214_189 18900001 19010000
AP008214_190 19000001 19110000

Query Match      80.0%; Score 16; DB 15; Length 110000;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      5  TGGTTGGGCAACACAT 20
      |||||
Db      67577 TGGTTGGGCAACACAT 67592

RESULT 44
AC097534
LOCUS      AC097534      139455 bp      DNA      linear      PRI 01-MAR-2002
DEFINITION Homo sapiens BAC clone RP11-798M19 from 4, complete sequence.
ACCESSION      AC097534      AC022744
VERSION      AC097534.3      GI:16874920
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (bases 1 to 139455)
AUTHORS      Sulston,J.E. and Waterston,R.
TITLE      Toward a complete human genome sequence
JOURNAL      Genome Res. 8 (11), 1097-1108 (1998)
PUBMED      9847074
REFERENCE      2 (bases 1 to 139455)
AUTHORS      Cedroni,M., Haakenson,W. and Creason,K.
TITLE      The sequence of Homo sapiens BAC clone RP11-798M19
JOURNAL      Unpublished (2001)
REFERENCE      3 (bases 1 to 139455)
AUTHORS      Waterston,R.H.
TITLE      Direct Submission
JOURNAL      Submitted (18-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE      4 (bases 1 to 139455)
AUTHORS      Waterston,R.H.
TITLE      Direct Submission
JOURNAL      Submitted (09-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE      5 (bases 1 to 139455)
AUTHORS      Waterston,R.H.
TITLE      Direct Submission
JOURNAL      Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE      6 (bases 1 to 139455)
AUTHORS      Waterston,R.
TITLE      Direct Submission
JOURNAL      Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 9, 2001 this sequence version replaced gi:16604096.
COMMENT      ----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0798M19
Drafting Center: WIBR
-----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
```

clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

**MAPPING INFORMATION:**

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/qsc>

**SOURCE INFORMATION:**

The RPI-11 human BAC library was made from the blood of one male donor, as described by Goegawa, K., Moon, P. Y., Zhao, B., Reagen, E., Taten, M., Catanes, J. and de Jong, P. J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.reagen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

**NEIGHBORING SEQUENCE INFORMATION:**

The clone sequenced to the left is RP11-500A5; the clone sequenced to the right is RP11-489G11, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-798M19; actual end is at base position 37652 of RP11-489G11.

Data from AC09588 and AC022691 was used to finish this clone, AC097534.

The sequence of AC022744 has been incorporated into AC097534.

**FEATURES**  
**source**

Location/Qualifiers  
1. .139455

```

Location/Qualifiers
1..139455
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"

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map="4"
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/clone="RP11-798M19
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/clone_lib=
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2510. .2548

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/rpt_family:
2567      2608

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2367. .2608
/root familyv=" (TTTC) n"
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3513. .3543

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/rpt family="AT rich"
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4559. 4739

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/rpt_family="MIR"
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4897. .5120

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/rpt_family="MERL_type"
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5609. .5913  
/root family-

6139. 6216  
/ipc\_family="AU"

/rpt family=

6217. .6689

/rpt\_family=

6690.7435

/rpt\_family=

6811. .6832  
/mnt/family-112E -ichn

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/proc_family=
7512- 7819

```

```
/bin: /bin
/rpt family="All"
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7796. .7824

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/rpt family="AT ri
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7844- .9184

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/rpt_family="MER1_typ
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7886. .7980

repeat_region	/rpt_family="AT_rich" 10470. .10509 /rpt_family="MIR" 11543. .11602 /rpt_family="ERVk" 11565. .11610 /rpt_family="(TC)n" 11622. .11691 /rpt_family="CT-rich" 11935. .11952 /rpt_family="MIR" 11953. .12264 /rpt_family="Alu" 12665. .12409 /rpt_family="MIR" 12671. .12856 /rpt_family="L1" 12846. .12904 /rpt_family="(TG)n" 12898. .13198 /rpt_family="L1" 13717. .13815 /rpt_family="MIR" 14135. .14212 /rpt_family="Mariner" 14213. .14498 /rpt_family="MER2_type" 14508. .14534 /rpt_family="(T)n" 14673. .14689 /note="match to EST AI207460 (NID:g6361468)" 14675. .14689 /note="match to EST BG505352 (NID:g134668656)" 17415. .17448 /rpt_family="(TTTA)n" 17419. .17732 /rpt_family="Alu" 17787. .17855 /rpt_family="AT_rich" 17828. .18065 /rpt_family="L1" 18933. .19073 /rpt_family="CRI" 20455. .20660 /rpt_family="MIR" 20561. .20590 /rpt_family="AT_rich" 23002. .23033 /rpt_family="(ATTG)n" 23072. .23106 /rpt_family="AT_rich" 24108. .24794 /rpt_family="CRI" 25049. .25457 /rpt_family="MaLR" 25641. .25664 /rpt_family="AT_rich" 25668. .25970 /rpt_family="Alu" 27131. .27319 /note="match to EST BB837547 (NID:g102699525)" 27855. .28073 /rpt_family="ERV1" 28125. .28175 /rpt_family="ERV1" 28153. .28251 /rpt_family="ERV1" 28256. .28366 /rpt_family="ERV1" 29347. .29634 /rpt_family="Alu" 33123. .33294
---------------	---



	Query Match	80.0%; Score 16; DB 8; Length 139455;	
	Best Local Similarity	100.0%; Pred. No. 44;	
	Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	4	TGTTGGTGGCAACACA 19 	
Db	121340	TGTTGGTGGCAACACA 121355	
RESULT 45			
AP005741			
LOCUS		141257 bp DNA linear PLN 28-JUL-2004	
DEFINITION	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8,		
PAC clone:P0470H09.			
ACCESSION	AP005741		
VERSION	AP005741.3 GI:37573143		
KEYWORDS			
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Eukarya sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzeae; Oryza.		
REFERENCE	1		
AUTHORS	Sasaki,T., Matsumoto,T. and Katayose,Y.		
TITLE	Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, PAC clone:P0470H09		
JOURNAL	Published Only in Database (2002)		
REFERENCE	2 (bases 1 to 141257)		
AUTHORS	Sasaki,T., Matsumoto,T. and Katayose,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-SEP-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@iasaffrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7411, Fax:81-298-38-7468)		
COMMENT	On Oct 7, 2003 this sequence version replaced gi:30984152. Genes were predicted from the integrated results of the following: GENSCAN ( <a href="http://CCR-081.mit.edu/GENSCAN.html">http://CCR-081.mit.edu/GENSCAN.html</a> ), FGENESH ( <a href="http://www.softberry.com/">http://www.softberry.com/</a> ), GeneMark.hmm ( <a href="http://opal.biology.gatech.edu/GeneMark/">http://opal.biology.gatech.edu/GeneMark/</a> ), GlimmerM ( <a href="http://www.tigr.org/tdb/glimmer/glmr_form.html">http://www.tigr.org/tdb/glimmer/glmr_form.html</a> ), RicheHM ( <a href="http://rgp.dna.affrc.go.jp/RiceHM/">http://rgp.dna.affrc.go.jp/RiceHM/</a> ), SplicePredictor ( <a href="http://bioinformatics.iastate.edu/cgi-bin/sp.cgi">http://bioinformatics.iastate.edu/cgi-bin/sp.cgi</a> ), sim4 ( <a href="http://globin.cse.psu.edu/html/docs/sim4.html">http://globin.cse.psu.edu/html/docs/sim4.html</a> ), gap2 ( <a href="http://www.tigr.org/software/glimmer/">http://www.tigr.org/software/glimmer/</a> ), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr ( <a href="ftp://ncbi.nlm.nih.gov/blast/db">ftp://ncbi.nlm.nih.gov/blast/db</a> ) and the cDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0470H09 clone has an overlap with P0571B09 (DDBJ: AP005526) clone at 5' end and with P0015A04 (DDBJ: AP005740) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <a href="http://rgp.dna.affrc.go.jp/GenomeSeq.html">http://rgp.dna.affrc.go.jp/GenomeSeq.html</a> . Location/Qualifiers 1..141257 /organism="Oryza sativa (japonica cultivar-group)"		



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misc_feature 21602..24700
/gene="P0470H09.7"
/note="GAG-POL precursor RIRE2"
gene complement(25017..25478)
/gene="P0470H09.8"
misc_feature complement(25017..25478)
/gene="P0470H09.8"
/note="putative orf5 RIRE2"
gene complement(26210..26977)
/gene="P0470H09.9"
misc_feature complement(26210..26977)
/gene="P0470H09.9"
/note="putative orf4 RIRE2"
gene complement(27064..27960)
/gene="P0470H09.10"
misc_feature complement(27064..27960)
/gene="P0470H09.10"
/note="putative orf3 RIRE2"
gene 28982..29422
LTR 28982..29422
/gene="P0470H09.6"
/note="3' LTR"
gene 30371..34991
/gene="P0470H09.11"
mRNA join(<30371..30914,31173..31337,32008..32093,32908..33047,
33670..34279,34905..>34991)
/gene="P0470H09.11"
/note="start and end point are not identified"
CDS join(30371..30914,31173..31337,32008..32093,32908..33047,
33670..34279,34905..34991)
/gene="P0470H09.11"
/codon_start=1
/product="circumsporozoite protein-like protein"
/protein_id="BAD33858.1"
/db_xref="GI:50726282"
translation="MALAARAGELHNLGPAADSFCAARSRPSWSTARVGAASP
SRPPPSGHTSPAAARAEAEELGEVVRKLNRRRAVSAYRRKMPARGAGQRPV
DDLDVAHDLRLGVLHQLVPLRGQVPAVLPRYLRLAVASSKNTARWASNIERRIGL
SPWEAAKSNCKYKSTRWRVFTCTDSVLEHNDMPPEQFMKTHASMLAHSE
RKGRPPASAGAKDRAGLLLELLVYGFIFPFGNNGYLVRARFASDPDVGFS
KTFVKPYPSFSDKPEGRDPRVPCRVHDYRGASRPGPSRVVPGTGLSATRLTVSE
VHAGARVNGGRCGACFAEDAVRHAQPHSSRWTCACREGKRELASADPVA
EVAPTRLRGHGRREVEADGNGRRTAVASGANGDTSEGEHTGLMHRKGDEP
TARIQMDLGGILRRQPAAREGGNGDGRFGRARASTRLRESVAGVLOGGATP
SEAGDERASAGRGAEAMTTATAGRFCAERRHQQ"
gene complement(38381..42196)
/misc_feature complement(38381..42196)
/note="probably inactive due to including stop codon(s) in
CDS
pseudogene, Fourf gag/pol protein"
/pseudo
gene 53728..54078
mRNA <53728..>54078
/gene="P0470H09.13"
CDS 53728..54078
/note="start and end point are not identified"
/gene="P0470H09.13"
/note="predicted by GlimmerW etc."
/codon_start=1
/product="hypothetical protein"
/protein_id="BAD33859.1"

Query Match 80.0%; Score 16; DB 15; Length 141257;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 TGGTTGGGCAACACAT 20
|||||
Db 45858 TGGTTGGGCAACACAT 45873
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RESULT 46
AC093739/c
LOCUS
DEFINITION Homo sapiens chromosome 2 clone RP11-22A4, WORKING DRAFT SEQUENCE,
2 unordered pieces.
AC093739 AC019029
AC093739.1 GI:15529777
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
Waterston,R.H.
The sequence of Homo sapiens clone
2 (bases 1 to 154612)
Waterston,R.H.
Direct Submission
Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 10, 2001 this sequence version replaced gi:7230152.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Center project name: H_NH0022A04
Drafting center: WIBR
----- Summary Statistics -----
Sequencing vector: M13; 52%
Chemistry: Dye-primer ET; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 152111 bases at least Q40
Consensus quality: 152371 bases at least Q30
Consensus quality: 154464 bases at least Q20
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved
* 1 54124: contig of 54124 bp in length
* 54125 54224: gap of unknown length
* 54225 154612: contig of 100388 bp in length.
FEATURES
source
1. 154612
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-22A4"
1. 54124
/note="assembly_name:Contig8
clone_end:17
vector_side:right"
54125..54224
/estimated_length=unknown
54225..154612
/note="assembly_name:Contig9
clone_end:SP6

misc_feature
1. 54124
/note="assembly_name:Contig8
clone_end:17
vector_side:right"
54125..54224
/estimated_length=unknown
54225..154612
/note="assembly_name:Contig9
clone_end:SP6
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## ORIGIN vector\_side:left"

Query Match 80.0%; Score 16; DB 14; Length 154612;  
 Best Local Similarity 100.0%; Pred.No. 44;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAAC 16  
 |||||

Db 113017 GCTTTGGTTGGGCAAC 113002  
 |||||

RESULT 47  
 AC009311/c  
 LOCUS 160625 bp DNA linear PRI 21-APR-2005  
 DEFINITION Homo sapiens BAC clone RP11-311L3 from 2, complete sequence.

AC009311  
 AC009311 GI:10716649

VERSION HTG.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 160625)

AUTHORS Nguyen,C., Maupin,R., Hawkins,M. and Le,T.

TITLE The sequence of Homo sapiens BAC clone RP11-311L3

JOURNAL Unpublished (2001)

REFERENCE 2 (bases 1 to 160625)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (13-AUG-1999) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA

REFERENCE 3 (bases 1 to 160625)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (15-MAR-2000) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA

REFERENCE 4 (bases 1 to 160625)

AUTHORS Waterston,R.

TITLE Direct Submission

JOURNAL Submitted (07-OCT-2000) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 5 (bases 1 to 160625)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (25-MAR-2001) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA

REFERENCE 6 (bases 1 to 160625)

AUTHORS Waterston,R.

TITLE Direct Submission

JOURNAL Submitted (29-OCT-2002) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 7 (bases 1 to 160625)

AUTHORS Wilson,R.K.

TITLE Direct Submission

JOURNAL Submitted (21-APR-2005) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA

COMMENT On Oct 7, 2000 this sequence version replaced gi:7243908.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu>

Contact: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)

----- Summary Statistics

----- Center project name: H\_NH0311L03

NOTICE:

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate  
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by sequence  
 from more than one subclone; and the assembly was confirmed by  
 restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren,  
 Department of Genetics, Washington University, St. Louis MO. For  
 additional information about the map position of this sequence, see  
<http://genome.wustl.edu>

## SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male  
 donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,  
 Tatenio,M., Catanese,J.J. and de Jong,P.J. (1998) An improved  
 approach for construction of bacterial artificial chromosome  
 libraries, Genomics 51:1-8. The clone may be obtained either from  
 Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong  
 and coworkers at <http://www.chori.org>  
 VECTOR: pBACe3.6

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-52K24, 200 base pair  
 overlap. The clone sequenced to the right is RP11-502N7, 200 base  
 pair overlap. Actual start of this clone is at base position 1 of  
 RP11-311L3; actual end is at base position 160625 of RP11-311L3.

## FEATURES

## source

1..160625

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/chromosome="2"

/clone="RP11-311L3"

/clone\_lib="RPCI-11"

178..773

## misc\_feature

/note="CpG island (GC=67.8, o/e=0.80, #CpGs=56)"

/complement(9279..28668)

## gene

/gene="NMI"

## mRNA

complement(join(9279..9683,10434..10540,14292..14478,  
 14566..14672,17636..17798,20756..20851,21676..21762,  
 28401..28668))

## CDS

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complement(join(9501..9683,10434..10540,14292..14478,  
 14566..14672,17636..17798,20756..20851,21676..21756))

/notes="NMI"

/note="Homo sapiens N-myc (and STAT) interactor (NMI),  
 mRNA: H\_NH0311L03.1"

This gene was based on gi(4758813)"

/codon\_start=1

/product="unknown"

/protein\_id="AAV15066.1"

/db\_xref="GI:62822518"

/translation="MEADKDDTOILKEHSPDEFIKDQNKGLIDETTKNIQLKKEI  
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 GQALTEKEEVAAQNVVSMGHVQIQNVLEIATKPLNPGVGRFVYVEVSKMKN  
 VTETPLTREDQKLELSFSGNRNGGGEVDVDRQSGSAVITFEIGVADKILK  
 KKEYPIYNTQHRVTVPYTEIHLKKYQIFSGTSKRTVLLTGMEGIQMDEEVEDLI  
 NIHFQKXNGGGEVDVVKSLGQPHIAYPEE"

27754..28613

## misc\_feature

/note="CpG island (GC=62.9, o/e=0.79, #CpGs=72)"

34781..35193

## misc\_feature

/note="CpG island (GC=74.1, o/e=0.66, #CpGs=40)"

96399..118854

## gene

/gene="TNFAIP6"

## mRNA

join(96399..96568,102751..102888,104864..105025,  
 108828..109056,112357..112397,118172..118854)

/genes="TNFAIP6"

## CDS

join(96475..96568,102751..102888,104864..105025,  
 108828..109056,112357..112397,118172..118341)

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/ gene="TNFAIP6"
/ note="Homo sapiens tumor necrosis factor, alpha-induced
protein 6 (TNFAIP6), mRNA; H NH0311L03.2
This gene was based on gi(26051242)"
/ codon_start=1
/ product="unknown"
/ protein_id="AAV15067.1"
/ db_xref="GI:62822519"
/ translation="MILLIFLLWEDTQGFQKDGIFHNSIWLERAGVYHREARS
GKYUTYAAKAVCFEGHLYATYQLEARKIGFHVCAAGMAKRGVYPIVKGPN
CFQGTGIDYGLRNSRWDAYCYNPAKCEGGVFTDPKQIPKSPGFPNEYDQNI
CYWHLRYGQRHLISFLDFDLEDDPGCLADYVEIYDSYDVHGFVRCGDELDDI
LSTGNVMTLKLSDASVTAGGFIKYVAMD PVSKSSQKQNTTSTTGKNFLAGFSH
L"
misc_feature 147349..147620
/ note="CpG island (%GC=61.4, o/e=0.83, #CpGs=20)"
148566..149580
/ note="CpG island (%GC=65.1, o/e=0.88, #CpGs=84)"
ORIGIN

Query Match      80.0%; Score 16; DB 8; Length 160625;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTTTGGTTGGGCAAC 16
Db      121737  GCTTTGGTTGGGCAAC 121722

RESULT 48
AC009588/c
LOCUS      AC009588      156472 bp      DNA      linear      HTG 09-SEP-2000
DEFINITION Homo sapiens chromosome 4 clone RP11-297M24 map 4, WORKING DRAFT
SEQUENCE, 18 unordered pieces.
ACCESSION      AC009588
VERSION      AC009588.5  GI:10045234
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1 (bases 1 to 156472)
AUTHORS      Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE      Homo sapiens chromosome 4, clone RP11-297M24
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 156472)
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
               Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
               Castle,A., Cerny,J., Colangelo,M., Collins,S., Collamore,A.,
               Cooke,P., Dearellano,K., Depayre,S., Devon,K., Dewar,K.,
               Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
               Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
               Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
               Karatas,A., Lehoczy,J., Lien,C., Locke,K., Macdonald,P.,
               Marquis,N., McSwan,P., McGurk,A., McKernan,K., McLaughlin,J.,
               Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,
               Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
               Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
               Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
               Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
               Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
DIRECT SUBMISSION
TITLE      Submitted
JOURNAL      Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT      On Sep 9, 2000 this sequence version replaced gi:5850482.
               All repeats were identified using RepeatMasker:
               Smit, A.F.A. & Green, P. (1996-1997)
               http://ftp.genome.washington.edu/RM/RepeatMasker.html
               ----- Genome Center
               Center: Whitehead Institute/ MIT Center for Genome Research
               Center code: WIER
               Web site: http://www-seq.wi.mit.edu

```

```

Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1737
Center clone name: 297_M_24
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator-amersham; 4% of reads
Chemistry: Dye-terminator Big Dye; 96% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 156962 bases at least Q40
Consensus quality: 161562 bases at least Q30
Consensus quality: 163407 bases at least Q20
Insert size: 171000; agarose-fp
Insert size: 164772; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bas.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 17576: contig of 17576 bp in length
* 17577 17676: gap of 100 bp
* 17677 19324: contig of 1648 bp in length
* 19325 19424: gap of 100 bp
* 19425 59066: contig of 39642 bp in length
* 59067 59166: gap of 100 bp
* 59167 62314: contig of 3148 bp in length
* 62315 62414: gap of 100 bp
* 62415 65191: contig of 2777 bp in length
* 65192 65291: gap of 100 bp
* 65292 69715: contig of 4424 bp in length
* 69716 69815: gap of 100 bp
* 69816 74395: contig of 4580 bp in length
* 74396 74495: gap of 100 bp
* 74496 79903: contig of 5408 bp in length
* 79904 80003: gap of 100 bp
* 80004 85577: contig of 5574 bp in length
* 85578 85677: gap of 100 bp
* 85678 94570: contig of 8893 bp in length
* 94571 101824: contig of 7154 bp in length
* 101825 101924: gap of 100 bp
* 101925 108382: contig of 6458 bp in length
* 108383 117723: contig of 9241 bp in length
* 117724 117823: gap of 100 bp
* 117824 127631: contig of 9808 bp in length
* 127632 127731: gap of 100 bp
* 127732 138685: contig of 10954 bp in length
* 138686 138785: gap of 100 bp
* 138786 150114: contig of 11329 bp in length
* 150115 150214: gap of 100 bp
* 150215 164874: contig of 14660 bp in length
* 164875 164974: gap of 100 bp
* 164975 166472: contig of 1498 bp in length.
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             /clone_lib="RPC1-11 Human Male BAC"
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             /note="assembly_fragment
clone_end:SP6
vector_side:left"
17577..17676
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             source
             gap

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vector\_side:right"

ORIGIN

Query Match 80.0%; Score 16; DB 14; Length 166472;  
Best Local Similarity 100.0%; Pred. No. 43;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 TTGGTTGGGCAACACA 19  
|||||  
Db 106452 TTGGTTGGGCAACACA 106437  
RESULT 49  
BX537258 188776 bp DNA linear ROD 17-DEC-2004  
LOCUS Mouse DNA sequence from clone RP23-152P13 on chromosome 4 Contains  
DEFINITION a eukaryotic translation initiation factor 4E (Eif4e) pseudogene  
and a eukaryotic translation initiation factor 4A (Eif4a)  
pseudogene, complete sequence.  
ACCESSION BX537258  
VERSION BX537258.3 GI:45581000  
KEYWORDS HTG; Eif4a; Eif4e.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (Bases 1 to 188776)  
AUTHORS North,P., Leaves,N., Greystrong,J., Coppola,M., Manjunath,S.,  
Russell,E., Smith,M., Strachan,G., Tofts,C., Boal,E., Cobley,V.,  
Hunter,G., Kimberley,C., Thomas,D., Cave-Berry,L., Weston,P. and  
Botcherby,M.R.M.  
TITLE Direct Submission  
JOURNAL Submitted (16-DEC-2004) Mouse Sequencing Group, HGMP-RC, Hinxton,  
Cambridge, CB10 1SB, UK. E-mail enquiries:- mrbotche@hgmp.mrc.ac.uk  
or pnorth@hgmp.mrc.ac.uk  
REMARK HGMP-RC part of the UK Mouse Sequencing Consortium  
COMMENT On Mar 18, 2004 this sequence version replaced gi:32451244.  
----- Genome Center  
Center: UK Medical Research Council  
Center code: UK-MRC  
Web site: http://mrcseq.har.mrc.ac.uk  
Contact: mouseq@har.mrc.ac.uk  
-----

The following abbreviations are used to associate primary accession  
numbers given in the feature table with their source databases:  
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information  
on the WORMPEP database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep/RP23-152P13 is  
from the RPCI-23 Mouse BAC Library  
constructed by the group of Pieter de Jong.  
For further details see http://www.chori.org/bacpac/home.htm  
VECTOR: pBACe3.6  
Sequence from the Mouse Genome Sequencing Consortium whole genome  
shotgun may have been used to confirm this sequence. Sequence data  
from the whole genome shotgun alone has only been used where it has  
a phred quality of at least 30.  
This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one subclone, and the assembly was confirmed by restriction digest,  
except on the rare occasion of the clone being a YAC.

FEATURES  
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23439..24091  
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/note="match: proteins: Sw:P06730 Sw:P20415 Sw:P29338"  
gene  
CDS

gene	Sw:P48597 Sw:Q9NOT5 Tr:Q8C470 Tr:Q9DFS6 Tr:Q9W7E5" /pseudo /codon_start=1 /product="eukaryotic translation initiation factor 4E (Eif4e) pseudogene" complement(47863..49080) /locus_tag="RP23-152P13.2-001" /pseudo complement(47863..49080) /locus_tag="RP23-152P13.2-001" /note="match: proteins: Sw:P04765 Sw:P29562 Tr:AAH49915 Tr:AAHG3812 Tr:O42576 Tr:Q7ZU67 Tr:Q7ZX50 Tr:Q802C9" /pseudo /codon_start=1 /product="eukaryotic translation initiation factor 4A (Eif4a) pseudogene"	
CDS		
ORIGIN		
Query Match	80.0%; Score 16; DB 9; Length 188776;	
Best Local Similarity	100.0%; Pred. No. 43;	
Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 GCCTTGGTGGCAAC 16 	
Db	131236 GCCTTGGTGGCAAC 131251	
RESULT 50		
AC116953		
LOCUS	AC116953 193506 bp DNA linear ROD 25-NOV-2003	
DEFINITION	Mus musculus BAC clone RP23-119H17 from chromosome 7, complete sequence.	
ACCESSION	AC116953	
VERSION	AC116953.5 GI:37202265	
KEYWORDS	HTG.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 193506) VanBrunt,A. The sequence of Mus musculus BAC clone RP23-119H17 Unpublished (2001)	
AUTHORS	2 (bases 1 to 193506) Wilson,R. Sequencing of Mus musculus Unpublished (2001)	
JOURNAL	3 (bases 1 to 193506) McPherson,J.D. and Waterston,R.H. Direct Submission Submitted (03-APR-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	
REFERENCE	4 (bases 1 to 193506) Wilson,R.K. Direct Submission Submitted (06-SEP-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	
AUTHORS	5 (bases 1 to 193506) Wilson,R.K. Direct Submission Submitted (01-OCT-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	
JOURNAL	6 (bases 1 to 193506) Wilson,R. Direct Submission Submitted (25-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Oct 1, 2003 this sequence version replaced gi:34495087.	
REFERENCE	----- Genome Center Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu	

-----  
Contact: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)  
----- Summary Statistics  
Center project name: M\_BA0119H17  
-----

**NOTICE:** This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

**MAPPING INFORMATION:**

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

**SOURCE INFORMATION:**

The RPC1-23 BAC library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (<http://www.chori.org>) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>.

**NEIGHBORING SEQUENCE INFORMATION:**

This sequence is the entire insert of the clone.

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repeat_region 32462. .32655
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repeat_region 33109. .33317
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repeat_region 38880. .39273
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repeat_region 39577. .39893
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repeat_region 41222. .41609
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Query Match 80.0%; Score 16; DB 9; Length 193506;  
Best Local Similarity 100.0%; Pred.No. 43;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 138492 CTTGGTTGGCAACA 138507
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Search completed: May 8, 2006, 04:49:00  
Job time : 1875 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 00:53:47 ; Search time 675 Seconds  
(without alignments)  
197.472 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20

Sequence: 1 gcttggttggaacacacat 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 1

Total number of hits satisfying chosen parameters: 9993364

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N Geneseq 21.\*

1: Geneseqm1980s.\*

2: Geneseqm1990s.\*

3: Geneseqm2000s.\*

4: Geneseqm2001as.\*

5: Geneseqm2001bs.\*

6: Geneseqm2002as.\*

7: Geneseqm2002bs.\*

8: Geneseqm2003as.\*

9: Geneseqm2003bs.\*

10: Geneseqm2003cs.\*

11: Geneseqm2003ds.\*

12: Geneseqm2004as.\*

13: Geneseqm2004bs.\*

14: Geneseqm2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	20	100.0	20 12	ADN97882
2	20	100.0	20 12	ADN40818
3	20	100.0	254 5	AAS14337
4	20	100.0	520 10	ADK61538
5	20	100.0	578 10	ADP79645
6	20	100.0	2514 5	AAS85052
7	20	100.0	2827 10	ACC72829
8	20	100.0	2827 12	ADQ03121
9	20	100.0	3200 12	ADQ03123
10	20	100.0	3421 13	ADR83528
11	20	100.0	3517 6	ABS73280
12	20	100.0	3517 12	ADQ03122
13	20	100.0	4945 12	ADN97721
14	20	100.0	4945 12	ADN40657
15	20	100.0	5722 13	ACF87489
16	20	100.0	5722 13	ACF87572
17	20	100.0	5723 6	ABV94143
18	20	100.0	5723 12	ADN06031
19	20	100.0	5723 12	ADN97714

c 20	20	100.0	5723	12	ADN40650	Adn40650 Human for
c 21	20	100.0	5723	13	ACN39628	Acn39628 Tumour-as
c 22	20	100.0	5723	14	ADY14881	Ady14881 DNA encod
c 23	20	100.0	5769	10	ADF81591	Adf81591 Leukaemia
c 24	20	100.0	5833	5	AAS85053	Aas85053 DNA encod
c 25	19	95.0	20	12	ADN97750	Adn97750 Human fox
c 26	19	95.0	20	12	ADN97828	Adn97828 Human fox
c 27	19	95.0	20	12	ADN40686	Adn40686 Human fox
c 28	19	95.0	20	12	ADN40764	Adn40764 Human for
c 29	17	85.0	2000	6	ABZ16434	Abz16434 Arabidops
c 30	16	80.0	20	12	ADN97751	Adn97751 Human fox
c 31	16	80.0	20	12	ADN97829	Adn97829 Human fox
c 32	16	80.0	20	12	ADN40687	Adn40687 Human for
c 33	16	80.0	20	12	ADN40765	Adn40765 Human for
c 34	16	80.0	4106	4	AAL05051	Aal05051 Human rep
c 35	16	80.0	4106	4	ABL97944	Ab197944 Human tes
c 36	16	80.0	160198	10	ADL13962	Adl13962 Osteoarth
c 37	16	80.0	164772	10	ADL13904	Adl13904 Osteoarth
c 38	15	75.0	406	12	ADL88066	Adl88066 DNA up-re
c 39	15	75.0	406	12	ADL88067	Adl88067 DNA up-re
c 40	15	75.0	498	9	ACH45273	Ach45273 Human foe
c 41	15	75.0	574	4	AAK88397	Aak88397 Human dig
c 42	15	75.0	574	5	AAS39498	Aas39498 cDNA enco
c 43	15	75.0	574	9	ADB32224	Adb32224 Human nov
c 44	15	75.0	1263	5	AAS75868	Aas75868 DNA encod
c 45	15	75.0	1342	2	AAV31252	Aav31252 E. coli J
c 46	15	75.0	1550	11	ADM02861	Adm02861 Human cDN
c 47	15	75.0	1635	6	ABQ75898	Abq75898 Human ubi
c 48	15	75.0	1701	10	ADF03345	Adf03345 Bacterial
c 49	15	75.0	2154	8	ACA21214	Act21214 Prokaryot
c 50	15	75.0	2181	9	ADA32702	Ada32702 DNA encod
c 51	15	75.0	2550	4	AAH14878	Aah14878 Human cDN
c 52	15	75.0	3059	10	ADA53348	Ada53348 Human cod
c 53	15	75.0	3342	4	ABL23542	Ab123542 Drosophil
c 54	15	75.0	3366	4	ABL17225	Ab117225 Drosophil
c 55	15	75.0	3593	4	AAD02709	Aad02709 Murine B7
c 56	15	75.0	3593	5	AAD02774	Aad02774 Murine B7
c 57	15	75.0	3593	10	AAD51099	Aad51099 Murine B7
c 58	15	75.0	3593	10	ABT14004	Abt14004 Murine PD
c 59	15	75.0	3593	12	ADJ75888	Adj75888 Marker ge
c 60	15	75.0	3593	14	ADZ61822	Adz61822 Murine Pd
c 61	15	75.0	5205	12	ADJ95458	Adj95458 Human cDN
c 62	15	75.0	5205	13	ADS86880	Ad86880 cDNA enco
c 63	15	75.0	5205	14	ADZ75838	Adz75838 Human E3a
c 64	15	75.0	5466	11	AEA90301	Aea90301 Human NOV
c 65	15	75.0	5492	4	ABL17224	Ab117224 Drosophil
c 66	15	75.0	6308	12	ADJ95441	Adj95441 Human cDN
c 67	15	75.0	6308	13	ADS86863	Ad86863 cDNA enco
c 68	15	75.0	6308	14	ADZ75821	Adz75821 Human E3a
c 69	15	75.0	7648	12	AD116377	Ad116377 Human pro
c 70	15	75.0	7742	8	ABZ24689	Abz24689 Human cel
c 71	15	75.0	110000	2	AAT42063	Continuation (12 o
c 72	15	75.0	349980	13	ADT05649	Adt05649 Haemophil
c 73	14	70.0	20	12	ADP76896	Adp76896 Chimeric
c 74	14	70.0	20	12	ADP76326	Adp76326 Chimeric
c 75	14	70.0	20	12	ADP76474	Adp76474 Chimeric
c 76	14	70.0	20	12	ADP76296	Adp76296 Chimeric
c 77	14	70.0	20	12	ADP76342	Adp76342 Chimeric
c 78	14	70.0	20	12	ADP76371	Adp76371 Chimeric
c 79	14	70.0	20	12	ADP76928	Adp76928 Chimeric
c 80	14	70.0	88	10	ADB75728	Adb75728 Tomato pl
c 81	14	70.0	229	12	ADQ04357	Adq04357 Maize tra
c 82	14	70.0	231	12	ADQ04355	Adq04355 Maize tra
c 83	14	70.0	266	12	ADQ04374	Adq04374 Maize tra
c 84	14	70.0	296	12	ACH90349	Ach90349 Human gen
c 85	14	70.0	306	4	ABL21351	Ab121351 Drosophil
c 86	14	70.0	339	6	ABN16060	Abn16060 Human ORF
c 87	14	70.0	349	3	AAC22674	Aac22674 Human sec
c 88	14	70.0	404	12	ADQ04378	Adq04378 Maize tra
c 89	14	70.0	410	3	AZ61682	Az61682 cDNA enco
c 90	14	70.0	410	4	ACQ99615	Aac99615 Skin cell
c 91	14	70.0	419	12	ADQ04384	Adq04384 Maize tra
c 92	14	70.0	440	6	ABL34767	Ab134767 Murine cD

C 93	14	70.0	471	9	ACH43968	Ach43968 Human foe	166	14	70.0	2439	10	ADB72460	Adb72460 Human NFA	
C 94	14	70.0	504	12	ACH76649	Ach76649 Human foe	167	14	70.0	2439	10	ADB95970	Adb95970 Human NFA	
C 95	14	70.0	593	13	ACN60177	Acn60177 Cotton gy	C 168	14	70.0	2474	2	AAV65248	Aav65248 DNA encod	
C 96	14	70.0	593	14	ACL55202	Acl55202 Human col	169	14	70.0	2478	14	ADV43378	Adv43378 Human psy	
C 97	14	70.0	632	5	ABV57221	Abv57221 Human pro	170	14	70.0	2586	10	ADJ56367	Adj56367 Human cdn	
C 98	14	70.0	657	4	AAH07975	Aah07975 Human GDN	171	14	70.0	2743	2	AAT36867	Aat36867 Human tra	
C 99	14	70.0	723	10	ADB76212	Adb76212 Mouse Con	172	14	70.0	2743	4	AAH02897	Aah02897 Human ehe	
100	14	70.0	748	13	ADQ82535	Adq82535 Wild type	173	14	70.0	2743	8	ACC83319	Acc83319 NF-ATc is	
101	14	70.0	750	6	ABK24137	Abk24137 DNA encod	174	14	70.0	2749	2	AAQ86687	Aaq86687 Human NF-	
102	14	70.0	750	6	ABK24136	Abk24136 DNA encod	175	14	70.0	2750	3	AAQ29252	Aaq29252 Human nuc	
103	14	70.0	750	6	ABK24141	Abk24141 DNA encod	176	14	70.0	2751	5	AAF31710	Aaf31710 Human NF-	
104	14	70.0	750	6	ABK24127	Abk24127 DNA encod	177	14	70.0	2751	9	ADA64048	Ada64048 Human cyt	
105	14	70.0	750	6	ABK24130	Abk24130 DNA encod	178	14	70.0	2751	9	ADA66407	Ada66407 Human NF-	
106	14	70.0	753	13	ADQ82527	Adq82527 Wild type	179	14	70.0	2793	8	ABZ79982	Abz79982 Human NF-	
107	14	70.0	753	13	ADQ82525	Adq82525 Wild type	180	14	70.0	2853	2	AAQ84301	Aaq84301 Human NF-	
108	14	70.0	753	13	ADQ82515	Adq82515 Wild type	181	14	70.0	2935	3	AAA35062	Aaa35062 Human ade	
109	14	70.0	753	13	ADQ82524	Adq82524 Wild type	182	14	70.0	2935	3	AAF21184	Aaf21184 Human low	
C 110	14	70.0	801	12	ADO63486	Ado63486 Transcrip	183	14	70.0	2935	9	ADA02721	Ada02721 Human NFA	
111	14	70.0	816	13	ADS49135	Ads49135 Bacterial	184	14	70.0	2935	10	ADB72459	Adb72459 Human NFA	
112	14	70.0	825	10	ADB76210	Adb76210 Mouse Con	185	14	70.0	2935	10	ADB95969	Adb95969 Human NFA	
113	14	70.0	887	4	AAI35745	Aai35745 Human mus	186	14	70.0	2935	10	ABZ96878	Abz96878 Human nuc	
114	14	70.0	887	4	AAI35747	Aai35747 Human mus	187	14	70.0	2935	11	ABD20727	Abd20727 Human pul	
115	14	70.0	887	8	ABX58733	Abx58733 cDNA enco	188	14	70.0	3036	13	ADS48001	Ads48001 Bacterial	
116	14	70.0	887	8	ABX58735	Abx58735 cDNA enco	189	14	70.0	3082	3	AAA30882	Aaa30882 Human GFA	
117	14	70.0	887	12	ADJ29485	Adj29485 Human mus	190	14	70.0	3082	8	ABA00846	Abaa00846 GFAT rela	
118	14	70.0	887	12	ADJ29483	Adj29483 Human mus	191	14	70.0	3082	8	ABA00845	Abaa00845 GFAT rela	
119	14	70.0	921	4	AAI35746	Aai35746 Human mus	192	14	70.0	3082	10	ADB31352	Adb31352 Bicalutam	
120	14	70.0	921	8	ABX58734	Abx58734 cDNA enco	193	14	70.0	3082	10	ADE38372	Ade38372 Human pro	
121	14	70.0	921	12	ADJ29484	Adj29484 Human mus	194	14	70.0	3082	12	ADP79271	Adp79271 Human GFA	
122	14	70.0	1083	10	ADB76208	Adb76208 Mouse Con	195	14	70.0	3082	12	ADQ15105	Adq15105 Human can	
C 123	14	70.0	1157	5	AA900006	Aa900006 DNA encod	196	14	70.0	3082	13	ADQ88169	Adq88169 Human 923	
124	14	70.0	1194	13	ADR91659	Adr91659 Novel S.	197	14	70.0	3082	13	ADP23395	Adp23395 PRO polyP	
125	14	70.0	1194	13	ADK45754	Adk45754 Streptoco	198	14	70.0	3082	14	ADZ70505	Adz70505 Human cdn	
126	14	70.0	1194	14	AEA55529	Aea55529 Streptoco	199	14	70.0	3082	14	ADZ75427	Adz75427 Human glu	
C 127	14	70.0	1275	8	ADA69899	Ada69899 Rice gene	200	14	70.0	3089	2	AAQ51188	Aaq51188 Human GFA	
C 128	14	70.0	1279	6	AAV27347	Aav27347 Streptoco	201	14	70.0	3136	8	ADA05761	Ada05761 Human NOV	
C 129	14	70.0	1279	6	ABQ84815	Abq84815 S. pneumo	202	14	70.0	3136	12	ADNG62925	Adng62925 Human NOV	
C 130	14	70.0	1279	10	ADC45128	Adc45128 S. pneumo	203	14	70.0	3140	14	ADY16380	Ady16380 DNA encod	
C 131	14	70.0	1281	10	ABX06032	Abx06032 S. pneumo	204	14	70.0	4152	12	ADL03974	Adl03974 DNA encod	
C 132	14	70.0	1284	2	AAK60295	Aak60295 DNA encod	C 205	14	70.0	4169	4	ABL28598	AbL28598 Drosophil	
C 133	14	70.0	1284	13	ADK44764	Adk44764 Streptoco	C 206	14	70.0	4539	4	AAH21113	Aah21113 C. glutam	
C 134	14	70.0	1308	13	ADR93018	Adr93018 Novel S.	207	14	70.0	4963	5	AAH78396	Aah78396 DNA encod	
C 135	14	70.0	1308	14	AEA56888	Aea56888 Streptoco	208	14	70.0	5030	4	ABL14824	AbL14824 Drosophil	
C 136	14	70.0	1375	5	AA573092	Aa573092 DNA encod	209	14	70.0	5358	4	ABL10596	AbL10596 Drosophil	
C 137	14	70.0	1448	11	ADP65415	Adp65415 Human ela	210	14	70.0	5403	2	AAV84140	Aav84140 Mouse pro	
C 138	14	70.0	1449	6	ABK35552	Abk35552 Gene Elas	211	14	70.0	5502	6	AAD34036	Aad34036 Human cyt	
C 139	14	70.0	1449	12	ADQ20799	Adq20799 Human sof	C 212	14	70.0	6555	5	AA94025	Aa94025 DNA encod	
140	14	70.0	1492	13	ADR60296	Adr60296 Cotton cd	213	14	70.0	8002	4	ABL10738	AbL10738 Drosophil	
141	14	70.0	1522	12	ADP04424	Adp04424 Sea squir	C 214	14	70.0	14283	4	ABL11798	AbL11798 Drosophil	
142	14	70.0	1588	8	ACA24312	Aca24312 Prokaryot	C 215	14	70.0	16995	2	AAV52215	Aav52215 Streptoco	
C 143	14	70.0	1599	13	ADX65230	Adx65230 Plant ful	216	14	70.0	17069	3	AAA35063	Aaa35063 Human ade	
C 144	14	70.0	1614	5	AA903035	Aa903035 DNA encod	217	14	70.0	17069	3	AAF21185	Aaf21185 Human low	
C 145	14	70.0	1992	5	AA569364	Aa569364 DNA encod	218	14	70.0	17069	10	ABZ96879	Abz96879 Human nuc	
146	14	70.0	2046	14	ADW23828	Adw23828 Novel hum	219	14	70.0	17069	11	ABD20728	Abd20728 Human pul	
147	14	70.0	2064	14	ADW23834	Adw23834 Novel hum	220	14	70.0	24526	6	AAD43979	Aad43979 Human tra	
148	14	70.0	2097	6	ABA93852	AbA93852 Human GFA	221	14	70.0	24526	13	ADU48434	Adu48434 Human tra	
149	14	70.0	2100	14	ADW23832	Adw23832 Novel hum	222	14	70.0	50927	13	ABD32585	Abd32585 Human can	
150	14	70.0	2118	14	ADW23838	Adw23838 Novel hum	C 223	14	70.0	80000	12	ADP49338	Adp49338 Human B-c	
151	14	70.0	2129	8	ABZ79986	Abz79986 Human NF-	C 224	14	70.0	89328	6	ABL61995	AbL61995 Colon ade	
C 152	14	70.0	2170	10	ADK67023	Adk67023 Gene #113	225	14	70.0	93390	10	ADD71350	Add71350 Glutamine	
C 153	14	70.0	2197	6	ABS73292	Abs73292 DNA encod	226	14	70.0	96596	10	AD895968	Ad895968 Human NFA	
C 154	14	70.0	2197	6	ABS73293	Abs73293 DNA encod	227	14	70.0	96597	9	ADA02720	Ada02720 Human NFA	
C 155	14	70.0	2197	13	ADR25367	Adr25367 Breast ca	228	14	70.0	96597	10	ADB72458	Adb72458 Human NFA	
C 156	14	70.0	2227	12	ADQ24524	Adq24524 Human sof	C 229	14	70.0	104729	12	ADQ18615	Adq18615 Human sof	
C 157	14	70.0	2306	4	ABL21350	AbL21350 Drosophil	C 230	14	70.0	110000	10	ABS56454	AbS56454 Continuation (3 of	
C 158	14	70.0	2360	12	ADK70354	Adk70354 Respirato	C 231	14	70.0	137908	11	ADP65634	Adp65634 Human seq	
C 159	14	70.0	2393	4	AAH99742	Aah99742 Human pro	C 232	14	70.0	201239	8	ACA64924	Aca64924 Human PLZ	
C 160	14	70.0	2406	5	ABV29515	Abv29515 Human pro	C 233	14	70.0	65.0	20	12	ADP76645	Adp76645 Chimeric
C 161	14	70.0	2407	5	AA587932	Aa587932 DNA encod	C 234	13	65.0	20	12	ADP77259	Adp77259 Chimeric	
C 162	14	70.0	2407	5	ABV27136	Abv27136 Human pro	C 235	13	65.0	24	2	AAV48170	Aav48170 Nucleotid	
C 163	14	70.0	2407	5	ABV21317	Abv21317 Human pro	C 236	13	65.0	28	10	ADC40569	Adc40569 Glucosami	
C 164	14	70.0	2407	5	ABV23653	Abv23653 Human pro	C 237	13	65.0	60	6	ABN38974	Abn38974 Human spl	
165	14	70.0	2439	9	ADA02722	Ada02722 Human NFA	C 238	13	65.0	100	8	ACD78689	AcD78689 E. coli K	



C 239	13	65.0	143	4	AAS49461	Aaa49461 Staphyloc	312	13	65.0	1131	12	ADL02574	Adl02574 DNA encod
C 240	13	65.0	143	8	ACA16698	Aac16698 Prokaryot	313	13	65.0	1134	2	AAQ40878	Aaq40878 Apyrase (
C 241	13	65.0	161	2	ART38771	Aat38771 Susceptib	314	13	65.0	1134	2	AAQ64128	Aaq64128 Virulence
C 242	13	65.0	168	9	ADA73541	Ada73541 Carcinoma	315	13	65.0	1140	8	ACA46309	Ac46309 Prokaryot
C 243	13	65.0	168	9	ADA73541	Ada73541 Mouse car	316	13	65.0	1140	10	ADD35786	Add35786 Human hep
C 244	13	65.0	168	10	ADB71734	Adb71734 Mouse car	317	13	65.0	1142	8	ACF72475	Acf72475 Staphyloc
C 245	13	65.0	216	3	AA243252	Aax43252 C. elegan	318	13	65.0	1152	4	ACS55148	Acs55148 Staphyloc
C 246	13	65.0	289	6	ABL84279	Abi84279 Human ova	319	13	65.0	1155	4	AAS54909	Aas54909 Staphyloc
C 247	13	65.0	300	3	AAAO0151	Aa00151 Human col	320	13	65.0	1161	2	AAV74808	Aav74808 Staphyloc
C 248	13	65.0	353	4	AAS49562	Aas49562 Staphyloc	321	13	65.0	1163	13	ADX47334	Adx47334 Plant ful
C 249	13	65.0	353	4	ACA16834	Aca16834 Prokaryot	322	13	65.0	1181	14	AEBA9671	Aeb9671 N. mening
C 250	13	65.0	362	5	ABA11932	Abal1932 Human ner	323	13	65.0	1182	2	AAZ12351	Aaz12351 Neisseria
C 251	13	65.0	377	6	ABN77863	Abn77863 Human ORF	324	13	65.0	1182	3	AAA81431	Aaa81431 N. mening
C 252	13	65.0	400	2	AAV77282	Aav77282 Staphyloc	325	13	65.0	1186	13	ADT19522	Adt19522 Plant cDN
C 253	13	65.0	408	2	AAK57731	Aax57731 Oligonuc	326	13	65.0	1226	6	ABQ68310	Abq68310 Listeria
C 254	13	65.0	418	8	ABX64948	Abx64948 Human gen	327	13	65.0	1260	13	ADK43765	Adk43765 Streptoco
C 255	13	65.0	445	14	ADW05800	Adw05800 Human gen	328	13	65.0	1277	13	ADX61590	Adx61590 Plant ful
C 256	13	65.0	476	13	ADT45177	Adt45177 Bacterial	329	13	65.0	1281	13	ADR93214	Adr93214 Novel S.
C 257	13	65.0	475	4	AAK56909	Aak56909 Human imm	330	13	65.0	1281	14	AEA57084	Aea57084 Streptoco
C 258	13	65.0	486	14	ADW05801	Adw05801 Human gen	331	13	65.0	1288	10	ADC87210	Adc87210 Human GPC
C 259	13	65.0	495	6	ABV98888	Abv98888 Human pan	332	13	65.0	1305	8	ACF72802	Acf72802 Staphyloc
C 260	13	65.0	522	10	ADK11955	Adk11955 Breast ca	333	13	65.0	1316	5	AAS69381	Aas69381 DNA encod
C 261	13	65.0	526	12	ACH67649	Ach67649 Human gen	334	13	65.0	1343	9	ADB83127	Adb83127 Human cDN
C 262	13	65.0	529	6	ABK46029	Abk46029 cDNA enco	335	13	65.0	1344	6	ABL57731	Abi57731 Human sbg
C 263	13	65.0	543	8	AA296358	Aaz96358 S. pneumo	336	13	65.0	1348	8	ABX71176	Abx71176 Novel hum
C 264	13	65.0	558	8	ACA34267	Aca34267 Prokaryot	337	13	65.0	1380	13	ADT46288	Adt46288 Bacterial
C 265	13	65.0	559	6	ABV95573	Abv95573 Human pan	338	13	65.0	1386	8	ACA46253	Ac46253 Prokaryot
C 266	13	65.0	580	12	ACH68503	Ach68503 Human gen	339	13	65.0	1407	12	ADL03054	Adl03054 DNA encod
C 267	13	65.0	599	4	AHA12948	Aah12948 Human cDN	340	13	65.0	1464	13	ADS46754	Ads46754 Bacterial
C 268	13	65.0	603	12	ADL04167	Adl04167 DNA encod	341	13	65.0	1475	2	AAV00528	Aav00528 HIV-1 bre
C 269	13	65.0	609	11	ABD09930	Abd09930 Pseudomon	342	13	65.0	1475	2	AAV00527	Aav00527 HIV-1 bre
C 270	13	65.0	617	4	AAH49182	Aah49182 P. patens	343	13	65.0	1475	10	AAD60069	Aad60069 HIV gp120
C 271	13	65.0	648	4	AHH04850	Aah04850 Human cDN	344	13	65.0	1475	10	AAD60070	Aad60070 HIV gp120
C 272	13	65.0	655	6	ABN77195	Abn77195 Human ORF	345	13	65.0	1475	12	ADK19366	Adk19366 HIV DNA e
C 273	13	65.0	694	4	AAH44255	Aah44255 Phycomit	346	13	65.0	1475	12	ADK19364	Adk19364 HIV DNA e
C 274	13	65.0	717	4	ABL17863	Abi17863 Phycophil	347	13	65.0	1491	5	AAS73196	Aas73196 DNA encod
C 275	13	65.0	741	13	ADS57498	Ads57498 Bacterial	348	13	65.0	1502	6	ADI16487	Adi16487 Human NOV
C 276	13	65.0	741	13	ADS57346	Ads57346 Bacterial	349	13	65.0	1502	12	ADN42143	Adn42143 Human cDN
C 277	13	65.0	750	13	ADT42758	Adt42758 Bacterial	350	13	65.0	1512	6	ABL42100	Abi42100 Nucleotid
C 278	13	65.0	752	9	ADB82339	Adb82339 Human cDN	351	13	65.0	1548	13	ADT15851	Adt15851 Plant cDN
C 279	13	65.0	776	4	AAI24293	Aai24293 Human bre	352	13	65.0	1550	4	AAF94450	Aaf94450 Human hyd
C 280	13	65.0	776	6	ABQ89396	Abq89396 Human pro	353	13	65.0	1584	10	ACC61436	Acc61436 Gene sequ
C 281	13	65.0	817	6	AAH32390	Aah32390 Human olf	354	13	65.0	1584	10	ADK63311	Adk63311 Disease t
C 282	13	65.0	830	13	ADX10461	Adx10461 Plant ful	355	13	65.0	1584	13	ADS46992	Ads46992 Bacterial
C 283	13	65.0	831	11	ABD09984	Abd09984 Pseudomon	356	13	65.0	1596	12	ADJ42314	Adj42314 Plant cDN
C 284	13	65.0	849	8	ADA68405	Ada68405 Arabidops	357	13	65.0	1625	14	ADW69528	Adw69528 DNA encod
C 285	13	65.0	856	10	ADF14131	Adf14131 Human end	358	13	65.0	1626	14	ADW69532	Adw69532 DNA encod
C 286	13	65.0	857	6	ABQ89460	Abq89460 Human pro	359	13	65.0	1641	13	ADX53851	Adx53851 Plant ful
C 287	13	65.0	857	9	ADB82403	Adb82403 Human cDN	360	13	65.0	1649	4	AAS01472	Aas01472 Human sec
C 288	13	65.0	890	13	ADX60572	Adx60572 Plant ful	361	13	65.0	1659	10	ADC91584	Adc91584 E. faeciu
C 289	13	65.0	918	2	AAT28561	Aat28561 Bacterial	362	13	65.0	1695	13	ADU26320	Adu26320 mcp gene
C 290	13	65.0	918	4	ABA76986	Ab76986 Antibioti	363	13	65.0	1713	14	ABB86389	Abb86389 Nucleotid
C 291	13	65.0	927	3	AAA38871	Aaa38871 Escherich	364	13	65.0	1803	4	AAK94689	Aak94689 Human ful
C 292	13	65.0	927	6	ABL57730	Abi57730 Human sbg	365	13	65.0	1803	4	AAS52001	Aas52001 Staphyloc
C 293	13	65.0	927	10	ACF68045	Acf68045 Phototrab	366	13	65.0	1803	8	ACF73454	Acf73454 Staphyloc
C 294	13	65.0	942	10	ABZ77910	Abz77910 Human G p	367	13	65.0	1803	12	ADL31671	Adl31671 Full leng
C 295	13	65.0	963	11	ABD08767	Abd08767 Pseudomon	368	13	65.0	1806	8	ACA43794	Ac43794 Prokaryot
C 296	13	65.0	990	3	AAC33134	Aac33134 Arabidops	369	13	65.0	1806	8	ACA19993	Ac19993 Prokaryot
C 297	13	65.0	998	10	ADD35785	Adt35785 Human hep	370	13	65.0	1806	14	ADW94225	Adw94225 Staphyloc
C 298	13	65.0	1007	13	ADT14812	Adt14812 Plant cDN	371	13	65.0	1805	14	ADW94572	Adw94572 Profilera
C 299	13	65.0	1014	13	ADS14796	Adsl4796 Pseudomon	372	13	65.0	1818	12	ADI45250	Adi45250 Rice isop
C 300	13	65.0	1036	13	ADX63420	Adx63420 Plant ful	373	13	65.0	1824	4	AAS55037	Aas55037 Staphyloc
C 301	13	65.0	1041	2	AAT60569	Aat60569 Cotton fi	374	13	65.0	1824	4	AAAS4633	Aas4633 Staphyloc
C 302	13	65.0	1050	11	ABD08526	Abd08526 Pseudomon	375	13	65.0	1824	10	ADC40564	Adc40564 Glucosami
C 303	13	65.0	1063	6	ADH48895	Adh48895 NOV76 cod	376	13	65.0	1835	10	ACA20889	Ac20889 Prokaryot
C 304	13	65.0	1086	14	ABE66864	Aeb66864 Rice geno	377	13	65.0	1835	9	ACA20889	Ac20889 Prokaryot
C 305	13	65.0	1092	6	ABL60613	Abi60613 Maize SBM	378	13	65.0	1842	9	ADA29653	Ada29653 DNA encod
C 306	13	65.0	1092	6	ABS65646	Abs65646 Mouse JNK	379	13	65.0	1842	8	ADA70832	Ada70832 Rice gene
C 307	13	65.0	1096	4	AAK69138	Aak69138 Human imm	380	13	65.0	1970	8	ABQ69785	Abq69785 Listeria
C 308	13	65.0	1110	10	ADD35787	Adt35787 Human hep	381	13	65.0	2000	6	ABZ16923	Abz16923 Arabidops
C 309	13	65.0	1117	11	ACL37791	Acl37791 Rice stre	382	13	65.0	2001	8	ADA72894	Ada72894 Rice gene
C 310	13	65.0	1125	4	AAF94440	Aaf94440 Human hyd	383	13	65.0	2001	4	ABL17553	Abi17553 Drosophil
C 311	13	65.0	1129	6	AD33646	Ad33646 Human TRI	384	13	65.0	2031	6	ABQ67851	Abq67851 Listeria

c 385	13	65.0	2064	3	AA27001	Aaa27001 Human Zwn	458	13	65.0	4234	12	ADL12784	Adl12784 Human ste
c 386	13	65.0	2069	4	AAH15627	Aah15627 Human cdn	c 459	13	65.0	4238	4	AAI57866	Aai57866 Human pol
c 387	13	65.0	2089	4	AA526624	Aaa26624 Human gen	c 460	13	65.0	4254	4	AAI59652	Aai59652 Human pol
c 388	13	65.0	2089	8	ABX713973	Abx713973 Human nov	c 461	13	65.0	4254	4	AAI59651	Aai59651 Human pol
c 389	13	65.0	2093	6	AA598513	Abs98513 Human ace	c 462	13	65.0	4254	5	AAF87435	Aaf87435 Corynebac
c 390	13	65.0	2100	4	AA502502	Aaa02502 Human gen	c 463	13	65.0	4268	4	AAI57865	Aai57865 Human pol
c 391	13	65.0	2100	4	AA502503	Aaa02503 Human gen	c 464	13	65.0	4353	8	AB236286	Ab236286 Human sec
c 392	13	65.0	2100	4	AA502505	Aaa02505 Human gen	c 465	13	65.0	4353	8	AB236286	Ab236286 Human sec
c 393	13	65.0	2100	4	AA502506	Aaa02506 Human gen	c 466	13	65.0	4411	4	ABL07996	AbL07996 Drosophil
c 394	13	65.0	2100	4	AA502508	Aaa02508 Human gen	c 466	13	65.0	4515	4	ABL26764	AbL26764 Drosophil
c 395	13	65.0	2100	4	AA502504	Aaa02504 Human gen	c 467	13	65.0	4590	8	ACA44121	Aca44121 Prokaryot
c 396	13	65.0	2100	4	AA502501	Aaa02501 Human gen	c 468	13	65.0	4616	6	ABQ70917	AbQ70917 Listeria
c 397	13	65.0	2178	13	ADT16956	Adt16956 Plant cdn	c 469	13	65.0	4826	2	AAV74586	Aav74586 Staphyloc
c 398	13	65.0	2181	12	ADI56698	Adi56698 Rat hypot	c 470	13	65.0	5019	4	ABL12778	AbL12778 Drosophil
c 399	13	65.0	2311	4	AAF97939	Aaf97939 Human sec	c 471	13	65.0	5162	2	AAV69919	Aav69919 Expressio
c 400	13	65.0	2311	4	AAF97939	Aaf97939 Human sec	c 472	13	65.0	5162	2	AAV69922	Aav69922 Mutagenic
c 401	13	65.0	2351	10	ADF38036	Adf38036 Synchroni	c 473	13	65.0	5262	2	AAV69927	Aav69927 Promoter
c 402	13	65.0	2354	5	AA568605	Aaa68605 DNA encod	c 474	13	65.0	5356	12	ADN05169	Adn05169 Antispori
c 403	13	65.0	2357	4	ABL25244	AbL25244 Drosophil	c 475	13	65.0	5358	6	ABQ55064	AbQ55064 Human ova
c 404	13	65.0	2388	2	AAV84554	Aav84554 Human sec	c 476	13	65.0	5621	4	ABL28688	AbL28688 Drosophil
c 405	13	65.0	2388	9	ACH04838	Ach04838 Novel hum	c 477	13	65.0	5816	3	AAAC74484	Aac74484 Human ORF
c 406	13	65.0	2388	9	ACH04838	Ach04838 Novel hum	c 478	13	65.0	5817	12	ADQ18917	Adq18917 Human sof
c 407	13	65.0	2394	4	AAF97906	Aaf97906 Human cdn	c 479	13	65.0	5853	12	ADQ23292	Adq23292 Human sof
c 408	13	65.0	2465	4	ABL05921	AbL05921 Drosophil	c 480	13	65.0	5972	4	ABL05920	AbL05920 Drosophil
c 409	13	65.0	2469	12	ADQ64149	Adq64149 Novel hum	c 481	13	65.0	6069	6	ADH48743	Adh48743 NOV11B co
c 410	13	65.0	2502	11	ABD10052	Abd10052 Pseudomon	c 482	13	65.0	6157	6	ADH48745	Adh48745 NOV11C co
c 411	13	65.0	2598	5	AA585458	Aaa85458 DNA encod	c 483	13	65.0	6195	6	ADH48741	Adh48741 NOV11A co
c 412	13	65.0	2616	2	AAZ12353	Aaz12353 Neisseria	c 484	13	65.0	6254	4	AAI32720	Aai32720 Human gen
c 413	13	65.0	2667	2	AAZ12352	Aaz12352 Neisseria	c 485	13	65.0	6254	4	AAI32951	Aai32951 Human gen
c 414	13	65.0	2667	14	ABE49673	Aeb49673 N. mening	c 486	13	65.0	6287	5	ABA20058	AbA20058 Human ner
c 415	13	65.0	2687	4	AA559659	Aaa59659 Propionib	c 487	13	65.0	6360	2	AAQ20577	Aaq20577 Human cyt
c 416	13	65.0	2687	8	ACF64588	Acf64588 Propionib	c 488	13	65.0	6360	2	AAQ20577	Aaq20577 Human cyt
c 417	13	65.0	2717	4	ABL17862	AbL17862 Drosophil	c 489	13	65.0	6780	4	AAK78375	Aak78375 Human imm
c 418	13	65.0	2718	10	ACF68678	Acf68678 Phototrab	c 490	13	65.0	6835	4	ABL08054	AbL08054 Drosophil
c 419	13	65.0	2766	3	AAZ61582	Aaz61582 DNA encod	c 491	13	65.0	6850	2	AAV69920	Aav69920 Expressio
c 420	13	65.0	2769	2	AAZ12354	Aaz12354 Neisseria	c 492	13	65.0	6866	4	AAK70762	Aak70762 Human imm
c 421	13	65.0	2769	3	AAZ61581	Aaz61581 DNA encod	c 493	13	65.0	6866	4	AAK71754	Aak71754 Human imm
c 422	13	65.0	2769	3	AAZ61580	Aaz61580 DNA encod	c 494	13	65.0	7159	2	AAV74613	Aav74613 Staphyloc
c 423	13	65.0	2769	14	ABE49678	Aeb49678 N. gonorr	c 495	13	65.0	7239	10	ADJ56389	Adj56389 Human cdn
c 424	13	65.0	2787	10	ABZ40533	Abz40533 N. gonorr	c 496	13	65.0	7339	4	AAK70901	Aak70901 Human imm
c 425	13	65.0	2800	3	AA26884	Aaa26884 Essential	c 497	13	65.0	7555	4	ABL10108	AbL10108 Drosophil
c 426	13	65.0	2800	4	AAI91566	Aai91566 Staphyloc	c 498	13	65.0	7744	4	AAF83380	Aaf83380 P. chryso
c 427	13	65.0	2800	4	AA508035	Aaa08035 Staphyloc	c 499	13	65.0	7744	4	AAF83381	Aaf83381 P. chryso
c 428	13	65.0	2800	10	AD067413	Add67413 Antibacte	c 500	13	65.0	7911	4	ABL06366	AbL06366 Drosophil
c 429	13	65.0	2800	10	AD067413	Add67413 Antibacte	c 501	13	65.0	8094	4	ABL03834	AbL03834 Drosophil
c 430	13	65.0	2824	10	AD067413	Add67413 Antibacte	c 502	13	65.0	8112	6	ABS51395	Abs51395 cDNA enco
c 431	13	65.0	2850	10	ADC08254	Acd08254 Rice DNA	c 503	13	65.0	8955	14	ADW94117	Adw94117 Staphyloc
c 432	13	65.0	2880	1	AA992068	Aan92068 Human mus	c 504	13	65.0	10200	4	ABL14622	AbL14622 Drosophil
c 433	13	65.0	2880	1	AAQ02068	Aaq02068 Human mus	c 505	13	65.0	10645	4	ABL12965	AbL12965 Drosophil
c 434	13	65.0	2911	13	ACN42066	Acn42066 Human dia	c 506	13	65.0	11451	14	ADW94161	Adw94161 Staphyloc
c 435	13	65.0	2972	13	ACN42065	Acn42065 Human dia	c 507	13	65.0	12138	4	ABL15550	AbL15550 Drosophil
c 436	13	65.0	2999	12	ADP22459	Adp22459 Sea-squir	c 508	13	65.0	12138	4	ABL15542	AbL15542 Drosophil
c 437	13	65.0	3012	13	ADL06367	Adl06367 Robacco 3	c 509	13	65.0	12332	4	ABL10880	AbL10880 Drosophil
c 438	13	65.0	3309	4	ABL06367	AbL06367 Drosophil	c 510	13	65.0	14175	4	AAK27814	Aak27814 DNA encod
c 439	13	65.0	3366	3	AAH77852	Aac77852 Human can	c 511	13	65.0	14175	4	AAK78859	Aak78859 Human imm
c 440	13	65.0	3603	10	AD073123	Ade73123 Human cel	c 512	13	65.0	14175	10	ADB94617	AdB94617 Novel hum
c 441	13	65.0	3625	13	ACN39530	Acn39530 Tumour-as	c 513	13	65.0	15396	4	ABL07860	AbL07860 Drosophil
c 442	13	65.0	3697	3	AAI6321	Aai6321 Human pro	c 514	13	65.0	15580	4	AAK65434	Aak65434 Human imm
c 443	13	65.0	3753	4	AAK78376	Aak78376 Human imm	c 515	13	65.0	17084	4	AAK70764	Aak70764 Human imm
c 444	13	65.0	3897	6	ABL60615	AbL60615 Maize SBM	c 516	13	65.0	17084	4	AAK71755	Aak71755 Human imm
c 445	13	65.0	4001	4	ABL17552	AbL17552 Drosophil	c 517	13	65.0	20099	10	AB222599	Ab222599 Human Fl3
c 446	13	65.0	4001	4	ABL17552	AbL17552 Drosophil	c 518	13	65.0	21407	4	ABL28892	AbL28892 Drosophil
c 447	13	65.0	4001	10	AAI54262	Aai54262 Movable g	c 519	13	65.0	21732	4	AAK90176	Aak90176 Human dig
c 448	13	65.0	4025	6	ABN87866	Abn87866 Human ova	c 520	13	65.0	21732	5	AAK39820	Aak39820 Genomic s
c 449	13	65.0	4026	10	ADH28847	Adh28847 Human chr	c 521	13	65.0	21732	9	ADB32780	AdB32780 Human nov
c 450	13	65.0	4047	13	AD080446	Ad080446 Full leng	c 522	13	65.0	32036	11	ACN44196	Acn44196 Mouse gen
c 451	13	65.0	4169	3	AAA81516	Aaa81516 N. mening	c 523	13	65.0	32503	4	ABL12964	AbL12964 Drosophil
c 452	13	65.0	4190	4	AAH16024	Aah16024 Human cdn	c 524	13	65.0	35042	3	AAA81454	Aaa81454 N. mening
c 453	13	65.0	4190	11	ADP65660	Adp65660 Human, Si	c 525	13	65.0	35962	8	ABZ09862	Abz09862 Human 5'
c 454	13	65.0	4190	11	ADP65660	Adp65660 Human, Si	c 526	13	65.0	35962	10	ADL13478	AdL13478 Osteoarth
c 455	13	65.0	4190	12	ADP05438	Adp05438 Human k1a	c 527	13	65.0	35962	13	ADR52883	Adr52883 Drug ther
c 456	13	65.0	4190	13	ADP24145	Adp24145 PRO polyt	c 528	13	65.0	44325	9	ADA02960	Ada02960 Human DAD
c 457	13	65.0	4195	4	AAD09379	Aad09379 Human ves	c 529	13	65.0	44325	10	ADB72698	AdB72698 Human DAD
							c 530	13	65.0	44325	10	ADC85440	Adc85440 Human Dad

c 531	13	65.0	44325	12	ADM74555	Adm74555 Human car	c 604	13	65.0	110000	14	ABE85185_12	Continuation (13 o	
c 532	13	65.0	45588	14	ABE32417	AbE32417 Human gen	c 605	13	65.0	124164	12	ADH19244	Adh19244 Human 5-h	
c 533	13	65.0	46555	14	ABE96541	AbE96541 Human IL1	c 606	13	65.0	124165	12	ADH19246	Adh19246 Human 5-h	
c 534	13	65.0	51157	13	ABD32986	Abd32986 Mouse can	c 607	13	65.0	124167	12	ADF83402	Adf83402 Human 5-h	
c 535	13	65.0	51193	14	AEA61136	Aea61136 Human KIA	c 608	13	65.0	124167	12	ADH19240	Adh19240 Human 5-h	
c 536	13	65.0	59645	14	ABE32372	AbE32372 Human gen	c 609	13	65.0	133462	13	ABD32622	Abd32622 Mouse can	
c 537	13	65.0	61197	11	ACN45130	Acn45130 Human gen	c 610	13	65.0	140036	6	AA598600	AA598600 Human gen	
c 538	13	65.0	61588	11	ACN44894	Acn44894 Human gen	c 611	13	65.0	143601	8	ABZ22654	ABZ22654 Human epi	
c 539	13	65.0	70419	8	ADA056111	Ada056111 Human WNT	c 612	13	65.0	155937	12	ADQ19389	Adq19389 Human sof	
c 540	13	65.0	70419	9	ADA02473	Ada02473 Human WNT	c 613	13	65.0	161671	12	ADH30232	Adh30232 Human PLO	
c 541	13	65.0	70419	10	ADB72212	AdB72212 Human WNT	c 614	13	65.0	171398	14	ADZ13359	Adz13359 Human can	
c 542	13	65.0	71292	11	ACN45142	Acn45142 Human gen	c 615	13	65.0	177587	11	ACN44805	Acn44805 Human can	
c 543	13	65.0	71655	14	ADZ13303	Adz13303 Human can	c 616	13	65.0	177930	14	ADZ13195	Adz13195 Human can	
c 544	13	65.0	74407	14	ADZ12490	Adz12490 Human can	c 617	13	65.0	188053	13	ABD32778	Abd32778 Mouse can	
c 545	13	65.0	75576	13	ABD33217	Abd33217 Murine ca	c 618	13	65.0	191584	13	ABD33586	Abd33586 Human can	
c 546	13	65.0	76826	14	ABE33167_3	AbE33167_3 of	c 619	13	65.0	191584	14	ABE17302	ABE17302 Human GNA	
c 547	13	65.0	78025	14	ADZ13607	AdZ13607 Murine ca	c 620	13	65.0	197140	14	ABE17302	ABE17302 Human GNA	
c 548	13	65.0	78313	9	ADA02618	Ada02618 Human FYN	c 621	13	65.0	199377	10	ADC35071	AdC35071 Mouse gen	
c 549	13	65.0	78313	10	ADB72356	AdB72356 Human FYN	c 622	13	65.0	212231	11	ACN44598	Acn44598 Human gen	
c 550	13	65.0	78313	10	ADQ95866	AdQ95866 Human FYN	c 623	13	65.0	218336	8	ABQ76678	AbQ76678 Androgen	
c 551	13	65.0	79329	12	ADQ97506	AdQ97506 Mouse can	c 624	13	65.0	218336	8	ABQ76678	AbQ76678 Androgen	
c 552	13	65.0	80240	2	AAV83940	AAv83940 NC-Contig	c 625	13	65.0	218802	14	ADW98820	Adw98820 Human her	
c 553	13	65.0	80595	2	AAV83939	AAv83939 HC-Contig	c 626	13	65.0	227246	13	ABD33272	Abd33272 Human can	
c 554	13	65.0	83120	9	AAV57571	AAv57571 Human CGI	c 627	13	65.0	229354	6	ABQ74179	AbQ74179 Human cyt	
c 555	13	65.0	84539	6	ABL64158	AbL64158 Stomach c	c 628	13	65.0	233060	11	ACN43912	Acn43912 Mouse gen	
c 556	13	65.0	84539	10	ADL13479	AdL13479 Osteoarthritis	c 629	13	65.0	233060	11	ACN43912	Acn43912 Mouse gen	
c 557	13	65.0	87761	11	ADL27164	AdL27164 Human gen	c 630	13	65.0	234884	11	ACN44210	Acn44210 Human gen	
c 558	13	65.0	90442	9	ADA03077	Ada03077 Mouse mCG	c 631	13	65.0	249878	10	ACF65381	Acf65381 Photorhab	
c 559	13	65.0	90442	9	ADA66361	Ada66361 Mouse mCG	c 632	13	65.0	334462	10	ADC24763	AdC24763 Human wil	
c 560	13	65.0	90442	10	ADB72815	AdB72815 Mouse mCG	c 633	13	65.0	347814	12	ADQ59440	AdQ59440 Human can	
c 561	13	65.0	90442	10	ADC26997	AdC26997 Mouse car	c 634	13	65.0	349881	10	ADC86642	AdC86642 Human GPC	
c 562	13	65.0	90442	11	ADL27155	AdL27155 Mouse gen	c 635	13	65.0	349980	10	ADC87621	AdC87621 Human GPC	
c 563	13	65.0	92638	6	ABQ88096	AbQ88096 Human ost	c 636	13	65.0	349980	3	AAF21610	Aaf21610 Neisseria	
c 564	13	65.0	94529	9	ADA03086	Ada03086 Human hCG	c 637	12	60.0	20	20	20	AAQ95695	AAq95695 Primer A
c 565	13	65.0	94529	10	ADB72824	AdB72824 Human hCG	c 638	12	60.0	20	12	ADP76430	Adp76430 ChimERIC	
c 566	13	65.0	94531	8	ADA68659	Ada68659 Arabidops	c 639	12	60.0	20	12	ADP76391	Adp76391 ChimERIC	
c 567	13	65.0	95769	8	ABK12169	AbK12169 Human DNA	c 640	12	60.0	22	11	ADZ44862	Adz44862 Pear S-ge	
c 568	13	65.0	96929	4	AAF28550	Aaf28550 Genomic f	c 641	12	60.0	24	6	AA558797	AA558797 Primer fo	
c 569	13	65.0	100848	4	AAF28552	Aaf28552 Genomic f	c 642	12	60.0	24	6	AA558797	AA558797 Primer fo	
c 570	13	65.0	100848	2	AA42063_08	AA42063_08	c 643	12	60.0	24	6	AB553146	Ab553146 Human zns	
c 571	13	65.0	110000	2	AAA81489_1	AAA81489_1	c 644	12	60.0	25	9	AB553146	Ab553146 Human gal	
c 572	13	65.0	110000	3	AAA81489_3	AAA81489_3	c 645	12	60.0	25	9	AB553146	Ab553146 Human gal	
c 573	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 646	12	60.0	36	4	AB553146	Ab553146 Human gal	
c 574	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 647	12	60.0	36	4	AB553146	Ab553146 Human gal	
c 575	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 648	12	60.0	36	4	AB553146	Ab553146 Human gal	
c 576	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 649	12	60.0	40	6	AB553146	Ab553146 Human gal	
c 577	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 650	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 578	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 651	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 579	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 652	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 580	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 653	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 581	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 654	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 582	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 655	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 583	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 656	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 584	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 657	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 585	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 658	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 586	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 659	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 587	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 660	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 588	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 661	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 589	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 662	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 590	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 663	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 591	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 664	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 592	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 665	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 593	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 666	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 594	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 667	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 595	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 668	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 596	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 669	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 597	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 670	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 598	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 671	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 599	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 672	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 600	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 673	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 601	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 674	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 602	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 675	12	60.0	41	6	AB553146	Ab553146 Human gal	
c 603	13	65.0	110000	6	ABX08336_12	ABX08336_12	c 676	12	60.0	41	6	AB553146	Ab553146 Human gal	

677	12	60.0	214	10	ADG41500	Adg41500 Human res	750	12	60.0	380	5	ABV15136	Abv15136 Human pro
678	12	60.0	214	10	ADG41499	Adg41499 Human res	751	12	60.0	380	12	ADP94984	Adp94984 Cotton ex
679	12	60.0	214	11	ADI97273	Adi97273 Human res	752	12	60.0	381	13	ACF87055	Acf87055 Human SIR
680	12	60.0	214	11	ADI97274	Adi97274 Human res	753	12	60.0	384	6	ABN25213	Abn25213 Human ORF
681	12	60.0	216	8	ACC55311	Acc55311 Rice endo	754	12	60.0	387	8	ABX52954	Abx52954 Bovine ES
682	12	60.0	217	12	ADF08364	Adf08364 Subacute	755	12	60.0	387	8	ACA49501	Ac49501 Prokaryot
683	12	60.0	217	12	ADF08372	Adf08372 Subacute	756	12	60.0	387	8	ACA35276	Ac35276 Prokaryot
684	12	60.0	221	8	ACA13642	Ac413642 Prokaryot	757	12	60.0	387	8	ACA32075	Ac32075 Prokaryot
685	12	60.0	234	8	ACA14953	Ac14953 Prokaryot	758	12	60.0	388	4	AAI86483	Aai86483 Human pol
686	12	60.0	239	4	AAI68589	Aai68589 A. thalia	759	12	60.0	389	4	AAI81709	Aai81709 Human pol
687	12	60.0	245	3	AAO65871	Aao65871 Human sec	760	12	60.0	390	4	AAO56361	Aao56361 Salmonell
688	12	60.0	245	4	AAO68067	Aao68067 Corynebac	761	12	60.0	390	4	AAO52602	Aao52602 E. coli D
689	12	60.0	245	4	AAO79507	Aao79507 Human imm	762	12	60.0	390	4	AAO84620	Aao84620 E. coli g
690	12	60.0	246	4	AAO79508	Aao79508 Human imm	763	12	60.0	390	4	AAO84588	Aao84588 E. coli g
691	12	60.0	247	3	AAO20072	Aao20072 Human sec	764	12	60.0	390	5	AAO81470	Aao81470 Escherich
692	12	60.0	253	3	AAO21861	Aao21861 Human sec	765	12	60.0	390	8	ACA54229	Ac54229 Prokaryot
693	12	60.0	265	10	ABX85173	Abx85173 Corn ear-	766	12	60.0	390	8	ACA51680	Ac51680 Prokaryot
694	12	60.0	267	4	AAK61163	Aak61163 Human imm	767	12	60.0	390	8	ACA18721	Ac18721 Prokaryot
695	12	60.0	280	8	ACA14585	Ac414585 Prokaryot	768	12	60.0	391	4	AAI89269	Aai89269 Human pol
696	12	60.0	280	12	ADP93793	Adp93793 Cotton ex	769	12	60.0	391	6	ABL37254	Ab137254 Human col
697	12	60.0	281	12	ACH83377	Ach83377 Human gen	770	12	60.0	393	11	ACH97969	Ach97969 Klebsiell
698	12	60.0	283	5	ABV49985	Abv49985 Human pro	771	12	60.0	394	6	ABS97602	Ab97602 Human epo
699	12	60.0	287	6	ABN23203	Abn23203 Human ORF	772	12	60.0	395	4	AAO34999	Aao34999 Human mus
700	12	60.0	291	2	AAT90489	Aat90489 Ferredoxi	773	12	60.0	395	5	ABV10068	Abv10068 Human pro
701	12	60.0	296	6	ABL73316	Ab173316 Corn tass	774	12	60.0	395	8	ABX57987	Abx57987 cDNA enco
702	12	60.0	300	3	AAA00769	Aaa00769 Human col	775	12	60.0	395	9	ACH31164	Ach31164 Human bon
703	12	60.0	300	4	AAO60005	Aao60005 Human rep	776	12	60.0	395	12	ADJ27714	Adj27714 Human mus
704	12	60.0	300	4	ABL98570	Ab198570 Human tes	777	12	60.0	395	12	ADP92728	Adp92728 Cotton ex
705	12	60.0	302	13	ACN57337	Acn57337 Cotton gy	778	12	60.0	398	4	AAK63960	Aak63960 Human imm
706	12	60.0	303	12	ADJ03139	Adj03139 DNA enco	779	12	60.0	398	4	AAI85370	Aai85370 Human pol
707	12	60.0	304	6	ABN75795	Abn75795 Human ORF	780	12	60.0	398	6	ABK64159	Abk64159 Human ben
708	12	60.0	305	4	AAK62665	Aak62665 Human imm	781	12	60.0	399	8	ACA14813	Aca14813 Prokaryot
709	12	60.0	306	11	ACL29388	Acl29388 Rice abio	782	12	60.0	399	11	ACL33880	Acl33880 Rice abio
710	12	60.0	306	13	ACN57425	Acn57425 Cotton gy	783	12	60.0	400	4	AAH69460	Aah69460 Human cer
711	12	60.0	315	4	AAI87231	Aai87231 Human pol	784	12	60.0	402	5	AAH78481	Aah78481 DNA enco
712	12	60.0	316	4	AAK65706	Aak65706 Human imm	785	12	60.0	405	4	AAH70795	Aah70795 Human cer
713	12	60.0	316	4	AAK65705	Aak65705 Human imm	786	12	60.0	406	4	AAI85420	Aai85420 Human pol
714	12	60.0	318	3	AAA42115	Aaa42115 Human sec	787	12	60.0	406	8	ACA15328	Aca15328 Prokaryot
715	12	60.0	329	4	AAI84344	Aai84344 Human pol	788	12	60.0	410	4	AAI89973	Aai89973 Human pol
716	12	60.0	333	3	AAZ53273	Aaz53273 Neisseria	789	12	60.0	414	2	AAO56757	Aao56757 Mouse scf
717	12	60.0	333	3	AAZ53274	Aaz53274 Neisseria	790	12	60.0	414	4	AAI83648	Aai83648 Human pol
718	12	60.0	336	3	AAO5494	Aao5494 Human sec	791	12	60.0	418	4	AAK64095	Aak64095 Human imm
719	12	60.0	341	4	AAK60871	Aak60871 Human imm	792	12	60.0	419	4	AAI81000	Aai81000 Human pol
720	12	60.0	343	3	AAFI11224	Aafi11224 Fusarium	793	12	60.0	420	12	ADQ19997	Adq19997 Human sof
721	12	60.0	343	13	ADU55265	Adu55265 Fusarium	794	12	60.0	420	12	ADQ03163	Adq03163 Arabidops
722	12	60.0	343	14	ADP93268	Adp93268 Fusarium	795	12	60.0	421	5	ABV17982	Abv17982 Human pro
723	12	60.0	345	4	AAH72341	Aah72341 Human cer	796	12	60.0	422	5	AAO81899	Aao81899 DNA enco
724	12	60.0	346	4	AAI90751	Aai90751 Human pol	797	12	60.0	423	4	AAK71921	Aak71921 Human imm
725	12	60.0	346	4	AAI91700	Aai91700 Human pol	798	12	60.0	423	6	ABK79803	Abk79803 Bacillus
726	12	60.0	349	4	AAK61279	Aak61279 Human imm	799	12	60.0	423	9	ADA32293	Ada32293 DNA enco
727	12	60.0	350	10	ABX99144	Abx99144 Rice endo	800	12	60.0	424	4	AAI85344	Aai85344 Human pol
728	12	60.0	353	4	AAO58884	Aao58884 Human can	801	12	60.0	425	4	AAO58090	Aao58090 Human imm
729	12	60.0	354	5	ABV53871	Abv53871 Human pro	802	12	60.0	434	13	ACF91475	Acf91475 Human SIR
730	12	60.0	354	14	ADV66713	Adv66713 S. mansoni	803	12	60.0	435	13	ACF89166	Acf89166 Human SIR
731	12	60.0	355	4	AAK58942	Aak58942 Human imm	804	12	60.0	436	4	AAK56279	Aak56279 Human imm
732	12	60.0	360	3	AAO30892	Aao30892 Breast ca	805	12	60.0	436	4	AAK78778	Aak78778 Human imm
733	12	60.0	360	4	AAK74118	Aak74118 Human imm	806	12	60.0	438	8	ACA14646	Ac414646 Prokaryot
734	12	60.0	361	3	AAO28849	Aao28849 Human sec	807	12	60.0	438	8	ACA14480	Ac414480 Prokaryot
735	12	60.0	363	4	AAO22937	Aao22937 Human bre	808	12	60.0	439	4	AAO55333	Aao55333 Human imm
736	12	60.0	363	4	AAI14075	Aai14075 Human bre	809	12	60.0	439	5	AAO93324	Aao93324 Small int
737	12	60.0	364	4	AAI91421	Aai91421 Human pol	810	12	60.0	439	8	ABX53746	Abx53746 Bovine ES
738	12	60.0	364	10	ACD95033	Ac495033 Human col	811	12	60.0	440	4	AAO89024	Aao89024 Human dig
739	12	60.0	365	3	AAO29635	Aao29635 Human sec	812	12	60.0	440	4	AAO25089	Aao25089 Human bre
740	12	60.0	366	4	AAO24245	Aao24245 Human bre	813	12	60.0	445	4	AAH72933	Aah72933 Human cer
741	12	60.0	368	4	AAI89550	Aai89550 Human pol	814	12	60.0	447	10	ACF71485	Acf71485 Phototrab
742	12	60.0	370	4	AAI13598	Aai13598 Human bre	815	12	60.0	447	13	ADS57714	Ads57714 Bacterial
743	12	60.0	374	6	ABA91568	Ab491568 Expressed	816	12	60.0	447	13	ADX63517	Adx63517 Plant ful
744	12	60.0	374	10	ABX93676	Abx93676 Expressed	817	12	60.0	451	6	ABL36955	Ab136955 Human col
745	12	60.0	374	14	ADY86165	Ady86165 Human EG-	818	12	60.0	459	5	ABV33025	Abv33025 Human pro
746	12	60.0	376	8	ACA14924	Ac414924 Prokaryot	819	12	60.0	460	4	AAK82953	Aak82953 Human imm
747	12	60.0	378	4	AAI80786	Aai80786 Human pol	820	12	60.0	461	7	ADS72594	Ads72594 Human kid
748	12	60.0	378	10	ADB61417	Ad61417 Rat gene	821	12	60.0	461	7	ADW41448	Adw41448 cDNA elev
749	12	60.0	378	10	ADP46053	Adp46053 Rat gene	822	12	60.0	467	4	AAO34898	Aao34898 cDNA enco

823	12	60.0	467	4	AAG311242	AAG311242 Human cDN	896	12	60.0	532	13	ACN61187	ACN61187 Cotton gy
824	12	60.0	467	4	AA163876	AA163876 Human pol	897	12	60.0	533	4	AAK83024	AAK83024 Human imm
825	12	60.0	467	4	ABA06550	ABA06550 Human cDN	c 898	12	60.0	533	14	ADW06489	ADW06489 Human gen
826	12	60.0	467	5	ABG29720	ABG29720 Human end	c 899	12	60.0	535	4	AAK55209	AAK55209 Human imm
827	12	60.0	467	6	ABQ66566	ABQ66566 Human pol	c 900	12	60.0	536	3	AAA81614	AAA81614 N. mening
828	12	60.0	467	6	ABV83887	ABV83887 Human pol	c 901	12	60.0	536	5	AAK82589	AAK82589 DNA encod
829	12	60.0	467	10	ADC10588	ADC10588 Human cDN	c 902	12	60.0	537	13	ACN61887	ACN61887 Cotton gy
830	12	60.0	467	10	ADC46056	ADC46056 Human neo	c 903	12	60.0	538	4	AAK92758	AAK92758 Human cDN
831	12	60.0	467	12	ADM24427	ADM24427 Human PRO	c 904	12	60.0	538	12	ADL29185	ADL29185 3' end of
832	12	60.0	469	13	ADQ50191	ADQ50191 Novel can	c 905	12	60.0	539	13	ACN57081	ACN57081 Cotton gy
c 833	12	60.0	470	4	ABA58764	ABA58764 Human foe	906	12	60.0	540	4	AAK63674	AAK63674 Human imm
c 834	12	60.0	470	4	AAI38449	AAI38449 Probe #71	c 907	12	60.0	540	11	ACN90587	ACN90587 Breast ca
c 835	12	60.0	470	4	AAK32632	AAK32632 Human bon	c 908	12	60.0	541	6	ABN60829	ABN60829 Human can
c 836	12	60.0	470	4	ABK32347	ABK32347 Human liv	c 909	12	60.0	541	13	ACN62081	ACN62081 Cotton gy
c 837	12	60.0	470	5	ABV51019	ABV51019 Human pro	c 910	12	60.0	547	5	ABA12527	ABA12527 Human ner
c 838	12	60.0	470	6	ABS07423	ABS07423 Human gen	c 911	12	60.0	547	14	ACL55398	ACL55398 Human col
c 839	12	60.0	471	2	AAI91944	AAI91944 The tyros	c 912	12	60.0	548	4	AAK28362	AAK28362 Genomic s
840	12	60.0	471	8	ABZ51014	ABZ51014 Aspergill	c 913	12	60.0	548	10	ADGA1558	ADGA1558 Human res
841	12	60.0	472	3	AAK43528	AAK43528 Zea maye	c 914	12	60.0	548	11	ADI97332	ADI97332 Human res
c 842	12	60.0	472	8	ABV77097	ABV77097 Nucleotid	c 915	12	60.0	549	3	AAF08783	AAF08783 Fusarium
843	12	60.0	472	13	ADR60516	ADR60516 Cotton cd	c 916	12	60.0	549	13	ADU52824	ADU52824 Fusarium
844	12	60.0	474	9	ACH44968	ACH44968 Human foe	c 917	12	60.0	549	14	ADZ90827	ADZ90827 Fusarium
845	12	60.0	475	4	AAI13663	AAI13663 Probe #35	c 918	12	60.0	551	4	AAH12195	AAH12195 Human cDN
846	12	60.0	475	4	ABA55373	ABA55373 Human foe	c 919	12	60.0	552	4	AAH13224	AAH13224 Human cDN
847	12	60.0	475	4	AAI35021	AAI35021 Probe #37	c 920	12	60.0	552	13	ADV39614	ADV39614 Rat cardi
848	12	60.0	475	4	ABA44906	ABA44906 Human bre	c 921	12	60.0	554	8	ABZ56152	ABZ56152 Aspergill
849	12	60.0	475	4	ABR25100	ABR25100 Probe #35	c 922	12	60.0	554	13	ACN62221	ACN62221 Cotton gy
850	12	60.0	475	4	AAK29075	AAK29075 Human bon	c 923	12	60.0	556	8	ABZ54198	ABZ54198 Aspergill
851	12	60.0	475	4	AAK03615	AAK03615 Human bra	c 924	12	60.0	558	4	AAI17420	AAI17420 Probe #73
852	12	60.0	475	4	ABS28693	ABS28693 Human liv	c 925	12	60.0	558	4	ABA62344	ABA62344 Human foe
853	12	60.0	475	5	AAI03547	AAI03547 Probe #35	c 926	12	60.0	558	4	AAI42322	AAI42322 Probe #11
854	12	60.0	475	6	ABS03622	ABS03622 Human gen	c 927	12	60.0	558	4	ABA29685	ABA29685 Probe #81
c 855	12	60.0	476	5	ABV46359	ABV46359 Human pro	c 928	12	60.0	558	4	AAK36564	AAK36564 Human bon
856	12	60.0	476	12	ACH87106	ACH87106 Human gen	c 929	12	60.0	558	4	AAK10678	AAK10678 Human bra
c 857	12	60.0	477	11	ACL34623	ACL34623 Rice abio	c 930	12	60.0	558	6	ABR36218	ABR36218 Human liv
858	12	60.0	478	9	ACH27287	ACH27287 Human adu	c 931	12	60.0	558	4	ABR30561	ABR30561 Human col
859	12	60.0	479	9	ACH13654	ACH13654 Human adu	c 932	12	60.0	558	6	ABQ57140	ABQ57140 Human col
860	12	60.0	480	12	ACH91998	ACH91998 Human gen	c 933	12	60.0	559	4	AAH10484	AAH10484 Human cDN
c 861	12	60.0	483	4	AAK66440	AAK66440 Human imm	c 934	12	60.0	561	14	ACL63248	ACL63248 Human col
c 862	12	60.0	486	11	ABD12760	ABD12760 Pseudomon	c 935	12	60.0	562	4	AAH09290	AAH09290 Human cDN
863	12	60.0	488	5	ABA13210	ABA13210 Human ner	c 936	12	60.0	563	10	ADD34671	ADD34671 Mouse mit
864	12	60.0	489	4	AAI00608	AAI00608 Human rep	c 937	12	60.0	565	4	AAH06050	AAH06050 Human cDN
c 865	12	60.0	489	5	ABV47771	ABV47771 Human pro	c 938	12	60.0	566	10	ADE58572	ADE58572 Rat gene
866	12	60.0	491	3	AAK78321	AAK78321 Human can	c 939	12	60.0	567	13	ACN57746	ACN57746 Cotton gy
c 867	12	60.0	495	9	ACH44577	ACH44577 Human foe	c 940	12	60.0	568	12	ACH70705	ACH70705 Human gen
868	12	60.0	496	3	AAK78246	AAK78246 Human can	c 941	12	60.0	570	6	ABK73743	ABK73743 Bacillus
c 869	12	60.0	498	6	ABN96743	ABN96743 Gene #324	942	12	60.0	571	13	ADK35564	ADK35564 Plant ful
870	12	60.0	498	13	ACN62311	ACN62311 Cotton gy	c 943	12	60.0	572	13	ACF86088	ACF86088 Human SIR
871	12	60.0	500	3	AAK94641	AAK94641 Cat flea	c 944	12	60.0	572	13	ADQ57192	ADQ57192 Novel can
872	12	60.0	500	12	ACH78291	ACH78291 Human gen	c 945	12	60.0	574	13	ACN49095	ACN49095 Cotton pr
873	12	60.0	502	10	ADK59991	ADK59991 Plant DNA	c 946	12	60.0	577	13	ADQ55400	ADQ55400 Novel can
874	12	60.0	508	2	AAV69714	AAV69714 3' portio	c 947	12	60.0	579	2	AAK57730	AAK57730 Oligonuc
875	12	60.0	508	3	AAK95738	AAK95738 Human NBM	c 948	12	60.0	579	12	ADL03722	ADL03722 DNA encod
876	12	60.0	508	6	ABS53917	ABS53917 Human iEN	c 949	12	60.0	584	13	ACN55181	ACN55181 Cotton an
c 877	12	60.0	512	5	AAH97940	AAH97940 Murine 7-	c 950	12	60.0	584	13	ACN56616	ACN56616 Cotton gy
878	12	60.0	512	12	ACH73737	ACH73737 Human gen	c 951	12	60.0	585	4	AAK53396	AAK53396 Haemophil
c 879	12	60.0	513	12	ACH69069	ACH69069 Human gen	c 952	12	60.0	585	8	ACA34269	ACA34269 Prokaryot
c 880	12	60.0	514	5	ABV56118	ABV56118 Human pro	c 953	12	60.0	595	2	AAQ80337	AAQ80337 DNA fragm
c 881	12	60.0	516	12	ACH71989	ACH71989 Human gen	954	12	60.0	595	2	AAI92919	AAI92919 Promoter
c 882	12	60.0	516	14	ACL58553	ACL58553 Human col	c 955	12	60.0	596	2	AAV15045	AAV15045 Promoter
883	12	60.0	520	5	ABV53458	ABV53458 Human pro	c 956	12	60.0	596	4	AAK83023	AAK83023 Human imm
884	12	60.0	521	13	ACN58131	ACN58131 Cotton gy	c 957	12	60.0	596	4	AAK83022	AAK83022 Human imm
c 885	12	60.0	522	4	AAK27957	AAK27957 Novel cDN	c 958	12	60.0	598	10	ADBS1725	ADBS1725 Primary r
c 886	12	60.0	522	10	ADGA0861	ADGA0861 Human res	c 959	12	60.0	601	4	AAK82994	AAK82994 Human imm
c 887	12	60.0	522	11	ADI96635	ADI96635 Human res	c 960	12	60.0	602	5	ABV03264	ABV03264 Human pro
c 888	12	60.0	522	12	ACH77250	ACH77250 Human gen	c 961	12	60.0	602	6	ABK34955	ABK34955 Human cDN
889	12	60.0	524	5	ABA17793	ABA17793 Human ner	c 962	12	60.0	605	2	AAQ63593	AAQ63593 Lelystet
c 890	12	60.0	525	3	AAA82401	AAA82401 N. mening	c 963	12	60.0	605	5	ABA14040	ABA14040 Human ner
c 891	12	60.0	525	13	ADQ80349	ADQ80349 EST #39 c	964	12	60.0	606	2	AAI14393	AAI14393 PRRSV Lel
c 892	12	60.0	526	4	AAI71198	AAI71198 Corynebac	965	12	60.0	606	6	ABT76695	ABT76695 PRRS viru
893	12	60.0	529	12	ACH69677	ACH69677 Human gen	966	12	60.0	606	6	ABT76687	ABT76687 PRRS viru
894	12	60.0	531	4	ABL11263	ABL11263 Drosophil	c 967	12	60.0	606	6	ABT76692	ABT76692 PRRS viru
c 895	12	60.0	532	6	ABL36754	ABL36754 Human col	c 968	12	60.0	607	13	ADX51824	ADX51824 Plant ful

c 969 12 60.0 608 6 ABN64400 Human can  
970 12 60.0 610 11 ACN91572 Breast ca  
971 12 60.0 612 5 ABV41950 Human pro  
c 972 12 60.0 612 6 ABK30448 Human G-p  
973 12 60.0 614 5 ABV33573 Human pro  
974 12 60.0 614 5 ABV42493 Human pro  
c 975 12 60.0 615 3 AAA16210 Human col  
c 976 12 60.0 616 13 ADR60466 Cotton cd  
c 977 12 60.0 617 13 ACN57656 Cotton gy  
978 12 60.0 618 4 AAS42855 Human G P  
c 979 12 60.0 625 8 ACA13938 Prokaryot  
c 980 12 60.0 625 13 ADQ57160 Novel can  
981 12 60.0 626 10 ADD16075 cDNA (Seq  
c 982 12 60.0 628 13 ADX48103 Plant ful  
983 12 60.0 629 13 ADQ54385 Novel can  
c 984 12 60.0 629 13 ADX09341 Plant ful  
c 985 12 60.0 630 3 AAC44029 zea mays  
986 12 60.0 630 4 AAS27145 cDNA enco  
987 12 60.0 630 4 AAS30220 DNA enco  
988 12 60.0 630 6 ABN60052 Human can  
989 12 60.0 630 8 ACD01475 Human pol  
990 12 60.0 630 10 ADB93323 Human CDN  
c 991 12 60.0 633 11 ACN86193 Breast ca  
992 12 60.0 634 10 ADE09829 Novel DNA  
c 993 12 60.0 634 13 ADX11530 Plant ful  
994 12 60.0 635 5 ADL37561 Human ova  
995 12 60.0 635 5 ADI72418 Human ova  
996 12 60.0 636 3 AAF13811 Aspergill  
997 12 60.0 636 4 AAH52675 S. epider  
998 12 60.0 636 13 ADU57852 Aspergill  
999 12 60.0 636 14 ADZ95855 Aspergill  
c1000 12 60.0 637 13 ADX32579 Plant ful

## ALIGNMENTS

RESULT 1  
ADN97882  
ID ADN97882 standard; DNA; 20 BP.  
XX  
AC ADN97882;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Monkey foxhead box O1a sequence inhibitory oligo #1.  
XX  
KW ss; cytostatic; antidiabetic; foxhead box O1a inhibitor;  
KW foxhead box O1a; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
KW diabetes; H-ras gene; antisense; gene expression; primer.  
XX  
OS Synthetic.  
XX  
PN W02004031350-A2.  
XX  
PD 15-APR-2004.  
XX  
PF 25-SEP-2003; 2003WO-US030352.  
XX  
PR 26-SEP-2002; 2002US-00260203.  
XX  
PS (AMGE-) AMGEN INC.  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
XX WPI; 2004-330164/30.  
XX  
PT New compounds, particularly antisense oligonucleotides, targeted to a  
PT nucleic acid molecule encoding foxhead box O1a, useful for treating  
PT cancer, or type 2 diabetes.  
XX  
PS Example 25; SEQ ID NO 172; 146pp; English.

XX The invention relates to a compound 8-80 nucleobases in length targeted  
CC to a nucleic acid molecule encoding foxhead box O1a, where the compound  
CC is at least 70% complementary to a nucleic acid molecule encoding  
CC foxhead box O1a and modulates expression of foxhead box O1a by at least  
CC 10%. The compound is useful for treating an animal having a disease or  
CC condition associated with foxhead box O1a, e.g. a hyperproliferative  
CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This  
CC sequence corresponds to an oligonucleotide targeted to the monkey foxhead  
CC box O1a genes in order to inhibit gene expression.  
XX  
SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCTTTGGTTGGCAACACAT 20  
Db 1 GCTTTGGTTGGCAACACAT 20  
RESULT 2  
ADN40818  
ID ADN40818 standard; DNA; 20 BP.  
XX  
AC ADN40818;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Monkey foxhead box O1a DNA antisense oligonucleotide #1.  
XX  
KW Monkey; foxhead box O1a; ss; antisense oligonucleotide;  
KW phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
KW type 2 diabetes; cytostatic; antidiabetic.  
XX  
OS Primates.  
XX  
PN US2004097459-A1.  
XX  
PD 20-MAY-2004.  
XX  
PF 25-SEP-2003; 2003US-00671074.  
XX  
PR 26-SEP-2002; 2002US-00260203.  
XX  
PA (DOBI/) DOBIE K W.  
PA (SHAN/) BHANOT S.  
PA (VENI/) VENIANT-ELLISON M.  
PA (LIND/) LINDBERG R A.  
PA (SHUT/) SHUTTER J R.  
XX  
PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
XX WPI; 2004-389194/36.  
XX  
PT New compounds, particularly antisense oligonucleotides, targeted to a  
PT nucleic acid molecule encoding foxhead box O1a, useful for treating  
PT cancer, or type 2 diabetes.  
XX  
PS Example 25; SEQ ID NO 172; 80pp; English.  
XX  
CC The invention relates to a compound targeted to a nucleic acid molecule  
CC encoding the human foxhead box O1a polypeptide. The compound is an  
CC antisense oligonucleotide that specifically hybridizes with the nucleic  
CC acid and inhibits expression of the polypeptide. The antisense  
CC oligonucleotide comprises at least one modified internucleoside linkage  
CC, i.e. a phosphorothioate linkage, at least one modified sugar moiety,  
CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified  
CC nucleobase comprising a 5-methylcytosine. The antisense compounds are  
CC useful for modulating the expression of the human foxhead box O1a  
CC polypeptide and in preparation of a composition for treating

CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,  
CC and type 2 diabetes. This sequence represents an antisense  
CC oligonucleotide targeted to DNA encoding the monkey forkhead O1a  
CC polypeptide of the invention.

XX SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0;

Qy 1 GCTTTGGTTGGCACAACAT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 GCTTTGGTTGGCACAACAT 20

RESULT 3  
AAS14337/c  
ID AAS14337 standard; cDNA; 254 BP.

XX AC AAS14337;

XX DT 27-FEB-2002 (first entry)

XX DE Human endometriosis-related marker DD12.

XX KW Human; endometriosis-related marker; endometrial cell; DD12;  
XX differential display; antiinflammatory; ss.

XX OS Homo sapiens.

XX PN WO200162959-A2.

XX PD 30-AUG-2001.

XX PF 26-FEB-2001; 2001WO-CA000245.

XX PR 25-FEB-2000; 2000US-0185063P.

XX PR 17-AUG-2000; 2000US-0225745P.

XX PA (PROC-) PROCREA BIOSCIENCES INC.

XX PI Baban S, Bernard M, Cherry B, Gosselin D, Hugo P, Malette B;  
XX Miron P, Prive C, Shazand K;

XX WIPI; 2001-648220/74.

XX Determining likelihood of endometriosis in female subject, involves  
XX obtaining endometrial cell sample from the subject, and assaying the  
XX cells for the expression level of at least one endometriosis-related  
XX marker.

XX Claim 44; Page 56; 92pp; English.

XX The present invention relates to a method of determining the likelihood  
XX of endometriosis in a female subject. The method comprises obtaining a  
XX sample of endometrial cells from a female subject, and assaying for the  
XX expression level of at least one endometriosis-related marker. The  
XX endometriosis-related markers are identified by differential display and  
XX are referred to as DD1-DD16. The markers are differentially expressed in  
XX the endometrial cells of females with endometriosis compared to  
XX endometriosis-free females. The method is useful as a diagnostic method  
XX for the detection of endometriosis in a female subject. The method is  
XX more rapid, non-invasive, much less complicated, and much less costly  
XX than laparoscopy. In contrast to the currently-available methods, the  
XX method is suitable for direct measurement of expression levels of  
XX endometriosis-related genes that are expressed differentially in  
XX endometrial cells depending on the presence/absence of endometriosis and  
XX the stage of the disease with relatively high levels of sensitivity and  
XX specificity. AAS14326-AAS14341 represent the endometriosis-related  
XX markers (DD1-DD16) of the present invention

XX SQ Sequence 254 BP; 77 A; 52 C; 57 G; 68 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.096;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCACAACAT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 90 GCTTTGGTTGGCACAACAT 71

RESULT 4  
ADK61538  
ID ADK61538 standard; DNA; 520 BP.

XX AC ADK61538;

XX DT 06-MAY-2004 (first entry)

XX DE Ovarian cancer-related DNA #693 with altered ovarian cancer expression.

XX KW ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;  
XX gene expression; primer; cancer.

XX OS Homo sapiens.

XX PN WO2003068054-A2.

XX PD 21-AUG-2003.

XX PF 13-FEB-2003; 2003WO-US004688.

XX PR 13-FEB-2002; 2002US-0357031P.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.

XX PI Jazaeri AA, Boyd J, Liu ET;

XX WIPI; 2003-689589/65.

XX Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-  
XX like tumor by determining a pattern of expression in the ovarian tumor of  
XX several markers.

XX Disclosure; SEQ ID NO 708; 137pp; English.

XX The invention relates to a method of classifying an ovarian tumor as a  
XX BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a  
XX pattern of expression in the ovarian tumor of several markers given in  
XX the specification; and (2) comparing a similarity of the pattern of  
XX expression of the markers in the ovarian tumor to a pattern of expression  
XX of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-  
XX like or non-BRCA-like tumor. The method is useful for classifying an  
XX ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.  
XX This sequence corresponds to an ovarian cancer -related gene having an  
XX altered pattern of expression in ovarian cancer. (Note: The sequence data  
XX for this patent did not form part of the printed specification but was  
XX obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences).

XX SQ Sequence 520 BP; 119 A; 122 C; 135 G; 134 T; 0 U; 10 Other;

Query Match 100.0%; Score 20; DB 10; Length 520;  
Best Local Similarity 100.0%; Pred. No. 0.095;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCACAACAT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 163 GCTTTGGTTGGCACAACAT 182

RESULT 5  
ADF79645/c



```

ID ADP79645 standard; DNA; 578 BP.
XX AC
XX ADF79645;
XX DT
XX 26-FEB-2004 (first entry)
XX DE
XX Leukaemia-related DNA sequence #201.
XX KW
XX Cytostatic; Gene therapy; leukaemia; ss.
XX OS
XX Unidentified.
XX PN
XX WO2003039443-A2.
XX PD
XX 15-MAY-2003.
XX PF
XX 04-NOV-2002; 2002WO-EP012303.
XX PR
XX 05-NOV-2001; 2001EP-00126244.
XX PR
XX 30-APR-2002; 2002EP-00009758.
XX PA
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX PA
XX (UFLU-) UNIV LUDWIG MAXIMILIANS.
XX PA
XX (HAFE/) HAFERLACH T.
XX PA
XX (SCHO/) SCHOCH C.
XX PA
XX (KERN/) KERN W.
XX PI
XX Haferlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;
XX PI
XX Eils R, Brors B, Mergenthaler S;
XX DR
XX WPI; 2003-505037/47.
XX PT
XX Determining the subtype of leukemia cells and whether a patient sample
XX PT
XX contains leukemia cells or other cells, useful for treating leukemia,
XX PT
XX comprises determining the expression profile of a group of markers in a
XX PT
XX patient sample.
XX PS
XX Disclosure; SEQ ID NO 201; 2938pp; English.
XX CC
XX The present invention relates to a method (M1) for determining the
XX CC
XX subtype of leukaemia cells and whether a patient sample contains
XX CC
XX leukaemia cells. The method comprises determining the expression profile
XX CC
XX of a group of markers in a patient sample. The method is useful for
XX CC
XX determining the presence of leukaemia cells, its types or subtypes, and
XX CC
XX for the preparation of a medicament for treating leukaemia.
XX SQ
XX Sequence 578 BP; 153 A; 164 C; 137 G; 124 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 10; Length 578;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTTGGTTGGGCAACACAT 20
DB 437 GCCTTGGTTGGGCAACACAT 418
RESULT 6
AAS85052/C
ID AAS85052 standard; cDNA; 2514 BP.
XX AC
XX AAS85052;
XX DT
XX 13-FEB-2002 (first entry)
XX DE
XX DNA encoding novel human diagnostic protein #20856.
XX KW
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS
XX Homo sapiens.
XX PN
XX WO200175067-A2.
XX PD
ADP79645 standard; DNA; 578 BP.
XX AC
XX ADF79645;
XX DT
XX 26-FEB-2004 (first entry)
XX DE
XX Leukaemia-related DNA sequence #201.
XX KW
XX Cytostatic; Gene therapy; leukaemia; ss.
XX OS
XX Unidentified.
XX PN
XX WO2003039443-A2.
XX PD
XX 15-MAY-2003.
XX PF
XX 04-NOV-2002; 2002WO-EP012303.
XX PR
XX 05-NOV-2001; 2001EP-00126244.
XX PR
XX 30-APR-2002; 2002EP-00009758.
XX PA
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX PA
XX (UFLU-) UNIV LUDWIG MAXIMILIANS.
XX PA
XX (HAFE/) HAFERLACH T.
XX PA
XX (SCHO/) SCHOCH C.
XX PA
XX (KERN/) KERN W.
XX PI
XX Haferlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;
XX PI
XX Eils R, Brors B, Mergenthaler S;
XX DR
XX WPI; 2003-505037/47.
XX PT
XX Determining the subtype of leukemia cells and whether a patient sample
XX PT
XX contains leukemia cells or other cells, useful for treating leukemia,
XX PT
XX comprises determining the expression profile of a group of markers in a
XX PT
XX patient sample.
XX PS
XX Disclosure; SEQ ID NO 201; 2938pp; English.
XX CC
XX The present invention relates to a method (M1) for determining the
XX CC
XX subtype of leukaemia cells and whether a patient sample contains
XX CC
XX leukaemia cells. The method comprises determining the expression profile
XX CC
XX of a group of markers in a patient sample. The method is useful for
XX CC
XX determining the presence of leukaemia cells, its types or subtypes, and
XX CC
XX for the preparation of a medicament for treating leukaemia.
XX SQ
XX Sequence 578 BP; 153 A; 164 C; 137 G; 124 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 10; Length 578;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTTGGTTGGGCAACACAT 20
DB 437 GCCTTGGTTGGGCAACACAT 418
RESULT 6
AAS85052/C
ID AAS85052 standard; cDNA; 2514 BP.
XX AC
XX AAS85052;
XX DT
XX 13-FEB-2002 (first entry)
XX DE
XX DNA encoding novel human diagnostic protein #20856.
XX KW
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS
XX Homo sapiens.
XX PN
XX WO200175067-A2.
XX PD
11-OCT-2001.
XX PD
30-MAR-2001; 2001WO-US008631.
XX PF
31-MAR-2000; 2000US-00540217.
XX PR
23-AUG-2000; 2000US-00649167.
XX XX
XX (HYSE-) HYSEQ INC.
XX PA
XX Drmanac RT, Liu C, Tang YT;
XX PI
XX WPI; 2001-639362/73.
XX DR
XX P-PSDB; ABG20865.
XX XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX PT
XX diagnostics, forensics, gene mapping, identification of mutations
XX PT
XX responsible for genetic disorders or other traits and to assess
XX PT
XX biodiversity.
XX PS
XX Claim 1; SEQ ID NO 20856; 103pp; English.
XX CC
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX CC
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX CC
XX and in recombinant production of (II). The polynucleotides are also used
XX CC
XX in diagnostics as expressed sequence tags for identifying expressed
XX CC
XX genes. (I) is useful in gene therapy techniques to restore normal
XX CC
XX activity of (II) or to treat disease states involving (II). (II) is
XX CC
XX useful for generating antibodies against it, detecting or quantitating a
XX CC
XX polypeptide in tissue, as molecular weight markers and as a food
XX CC
XX supplement. (II) and its binding partners are useful in medical imaging
XX CC
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX CC
XX involving aberrant protein expression or biological actions in
XX CC
XX polypeptide and polynucleotide sequences have applications in
XX CC
XX diagnostics, forensics, gene mapping, identification of mutations
XX CC
XX responsible for genetic disorders or other traits to assess biodiversity
XX CC
XX and to produce other types of data and products dependent on DNA and
XX CC
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX CC
XX coding sequences of the invention. Note: The sequence data for this
XX CC
XX patent did not appear in the printed specification, but was obtained in
XX CC
XX electronic format directly from WIPO at
XX CC
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ
XX Sequence 2514 BP; 658 A; 738 C; 620 G; 498 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 5; Length 2514;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTTGGTTGGGCAACACAT 20
DB 2466 GCCTTGGTTGGGCAACACAT 2447
RESULT 7
ACC72829/C
ID ACC72829 standard; cDNA; 2827 BP.
XX AC
XX ACC72829;
XX XX
XX 09-JUL-2003 (first entry)
XX DT
XX Human cancer related protein encoding cDNA SEQ ID NO:167.
XX DE
XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
XX KW
XX heart disease; atherosclerosis; endometriosis; gene; ss.
XX KW
XX Homo sapiens.
XX OS
XX WO2003025138-A2.
XX PN
XX 27-MAR-2003.
XX PD
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XX 17-SEP-2002; 2002WO-US029560.  
 XX 17-SEP-2001; 2001US-0323469P.  
 PR 20-SEP-2001; 2001US-0323887P.  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 08-FEB-2002; 2002US-0355145P.  
 PR 08-FEB-2002; 2002US-0355257P.  
 PR 12-APR-2002; 2002US-0372246P.  
 XX (EOSB-) EOS BIOTECHNOLOGY INC.  
 PA Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KB;  
 PI Zlotnik A;  
 XX WPI; 2003-354600/33.  
 DR P-PSDB; ABR58678.  
 XX New genes that are up-regulated or down-regulated in cancers, useful as  
 PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as  
 PT therapeutic targets for screening drugs for treating these diseases.  
 XX  
 PS Claim 8; Page 718-719; 767pp; English.  
 PS  
 CC The present invention describes an isolated nucleic acid molecule, which  
 CC comprises the sequence of any of the genes that are up-regulated or down-  
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in  
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer  
 CC related gene nucleotide sequences which encode the proteins given in  
 CC ABR58521 to ABR58709. Also described: (1) determining the presence or  
 CC absence of a pathological cell in a patient; (2) an expression vector  
 CC comprising a nucleic acid molecule described above; (3) a host cell  
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by  
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide  
 CC of (4); (6) specifically targeting a compound to a pathological cell in a  
 CC patient by administering to the patient the antibody above; and (7) a  
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or  
 CC therapeutic targets. In particular, the nucleic acid is useful for  
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,  
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,  
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,  
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in  
 CC drug screening, particularly for identifying agents for treating these  
 CC pathologies  
 XX  
 SQ Sequence 2827 BP; 732 A; 831 C; 693 G; 571 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 2827;  
 Best Local Similarity 100.0%; Pred. No. 0.093;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GCTTTGGTTGGCAACACAT 20  
 |||||  
 Db 2647 GCTTTGGTTGGCAACACAT 2628  
 RESULT 8  
 ADQ03121/c  
 ID ADQ03121 standard; DNA; 2827 BP.  
 XX  
 AC ADQ03121;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE PAX3-FKHR fusion gene translocation DNA seqid 1.  
 XX  
 KW fusion transcript identification; chromosome abnormality;  
 KW genetic disorder; degenerative disease; cancer; leukaemia;  
 KW chronic myelogenous leukaemia; CML; gene rearrangement; PAX3-FKHR;  
 KW translocation; Alveolar rhabdomyosarcoma; ARMS; BS;  
 KW expressed sequence tag; EST.  
 XX  
 OS Unidentified.

XX US2004110227-A1.  
 XX 10-JUN-2004.  
 XX 19-MAR-2003; 2003US-00391530.  
 XX 19-MAR-2002; 2002US-0365076P.  
 XX (LEVA/) LEVANON E.  
 PA (TOPO/) TOPORIK A.  
 PA (AKIV/) AKIVA P.  
 XX Levanon E, Toporik A, Akiva P;  
 PI WPI; 2004-532613/51.  
 DR  
 XX  
 PT Identifying putative fusion transcripts, by aligning first database of  
 PT annotated polynucleotide with database of expressed polynucleotide, and  
 PT identifying expressed polynucleotide complementary to non-contiguous  
 PT sequences of first database.  
 XX  
 PS Example 9; SEQ ID NO 1; 133pp; English.  
 PS  
 CC The invention describes a method of identifying (M1) putative fusion  
 CC transcripts. The method involves computationally aligning a first  
 CC database of annotated polynucleotide sequences with a second database of  
 CC expressed polynucleotide sequences, and identifying in the second  
 CC database an expressed polynucleotide sequence complementary to at least  
 CC two non-contiguous sequences (S1) of the first database, where the  
 CC expressed polynucleotide sequence identified is a putative fusion  
 CC transcript, and (S1) is chosen from non-homologous polynucleotide  
 CC sequences mapped to different chromosomes, polynucleotide sequences  
 CC mapped to different loci of a single chromosome and polynucleotide  
 CC sequences mapped to a single locus and not being a part of a splice  
 CC isoform, the expressed polynucleotide sequence identified is a putative  
 CC fusion transcript. (M1) is useful for identifying putative fusion  
 CC transcripts, for identifying transition points in fusion transcripts, for  
 CC identifying polynucleotide sequence associated with a disorder associated  
 CC with gene rearrangements, for identifying polypeptides resulting from  
 CC putative fusion events, for detecting nucleic acid sequence chimerism  
 CC indicative of predisposition for disorders associated with genetic  
 CC rearrangements, and for identifying putative mutagenic agents. (M1) is  
 CC useful for identifying gene rearrangements, chromosome abnormalities,  
 CC which are associated with genetic disorders, agents known to cause  
 CC degenerative diseases such as cancer e.g., leukaemia, chronic myelogenous  
 CC leukaemia (CML), and in diagnosis of various diseases related to gene  
 CC rearrangements. This sequence represents a PAX3-FKHR t(2;13)(q35;q14)  
 CC translocation polynucleotide associated with Alveolar rhabdomyosarcoma  
 CC (ARMS).  
 XX  
 SQ Sequence 2827 BP; 732 A; 831 C; 693 G; 571 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 12; Length 2827;  
 Best Local Similarity 100.0%; Pred. No. 0.093;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GCTTTGGTTGGCAACACAT 20  
 |||||  
 Db 2647 GCTTTGGTTGGCAACACAT 2628  
 RESULT 9  
 ADQ03123/c  
 ID ADQ03123 standard; DNA; 3200 BP.  
 XX  
 AC ADQ03123;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE PAX3-FKHR fusion gene translocation DNA seqid 3.  
 XX  
 KW fusion transcript identification; chromosome abnormality;

KW genetic disorder; degenerative disease; cancer; leukaemia;  
KW chronic myelogenous leukaemia; CML; gene rearrangement; PAX3-FKHR;  
KW translocation; Alveolar rhabdomyosarcoma; ARMS; BS;  
KW expressed sequence tag; EST.  
XX Homo sapiens.  
XX US2004110227-A1.  
XX 10-JUN-2004.  
XX 19-MAR-2003; 2003US-00391530.  
XX 19-MAR-2002; 2002US-0365076P.  
XX (LEVA/) LEVANON E.  
XX (TOPO/) TOPORIK A.  
XX (AKIV/) AKIVA P.  
XX Levanon E, Toporik A, Akiva P;  
XX WPI; 2004-532613/51.  
XX Identifying putative fusion transcripts, by aligning first database of  
XX annotated polynucleotide with database of expressed polynucleotide, and  
XX identifying expressed polynucleotide complementary to non-contiguous  
XX sequences of first database.  
XX Example 9; SEQ ID NO 3; 133pp; English.  
XX The invention describes a method of identifying (M1) putative fusion  
XX transcripts. The method involves computationally aligning a first  
XX database of annotated polynucleotide sequences with a second database of  
XX expressed polynucleotide sequences, and identifying in the second  
XX database an expressed polynucleotide sequence complementary to at least  
XX two non-contiguous sequences (S1) of the first database, where the  
XX expressed polynucleotide sequence identified is a putative fusion  
XX transcript, and (S1) is chosen from non-homologous polynucleotide  
XX sequences mapped to different chromosomes, polynucleotide sequences  
XX mapped to different loci of a single chromosome and polynucleotide  
XX sequences mapped to a single locus and not being a part of a splice  
XX isoform, the expressed polynucleotide sequence identified is a putative  
XX fusion transcript. (M1) is useful for identifying putative fusion  
XX transcripts, for identifying transition points in fusion transcripts, for  
XX identifying polynucleotide sequence associated with a disorder associated  
XX with gene rearrangements, for identifying polypeptides resulting from  
XX putative fusion events, for detecting nucleic acid sequence chimerism  
XX indicative of predisposition for disorders associated with genetic  
XX rearrangements, and for identifying putative mutagenic agents. (M1) is  
XX useful for identifying gene rearrangements, chromosome abnormalities,  
XX which are associated with genetic disorders, agents known to cause  
XX degenerative diseases such as cancer e.g., leukaemia, chronic myelogenous  
XX leukaemia (CML), and in diagnosis of various diseases related to gene  
XX rearrangements. This sequence represents a PAX3-FKHR t(2;13)(q35;q14)  
XX translocation polynucleotide associated with Alveolar rhabdomyosarcoma  
XX (ARMS).  
XX Sequence 3200 BP; 857 A; 869 C; 754 G; 720 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 3200;  
Best Local Similarity 100.0%; Pred. No. 0.092;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCCTTGGTTGGGCAACACAT 20  
DB 2511 GCCTTGGTTGGGCAACACAT 2492  
RESULT 10  
ADR83528/c  
ID ADR83528 standard; DNA; 3421 BP.  
XX AC ADR83528;

XX 02-DEC-2004 (first entry)  
XX Human fork head domain protein DNA, target gene of miRNA.  
XX human; ds; miRNA; microRNA; ontogenesis; cell therapy; cancer;  
KW immune disease; nerve disorder; amyotrophic lateral sclerosis;  
KW Parkinson's disease; Alzheimer's disease; inflammatory disease;  
KW siRNA silencing precursor; cytostatic; immunosuppressive; nootropic;  
KW neuroprotective; antiinflammatory; immunotherapy;  
KW fork head domain protein.  
XX Homo sapiens.  
XX WO2004076622-A2.  
XX 10-SEP-2004.  
XX 10-FEB-2004; 2004WO-JP001433.  
XX 10-FEB-2003; 2003US-0445829P.  
XX (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
XX Taira K, Kawasaki H;  
XX WPI; 2004-653393/63.  
XX Modulating expression of a target gene in a cell, for treating cancer, an  
XX immune disease, or a nerve disorder, comprises introducing into the cell  
XX a polynucleotide that forms a duplex region with an mRNA transcribed from  
XX the target gene.  
XX Claim 9; SEQ ID NO 430; 865pp; English.  
XX This invention relates to a novel method for modulating the expression of  
XX a target gene in a cell. Specifically, it refers to the introduction into  
XX a cell of a polynucleotide that forms a duplex region with an mRNA  
XX transcribed from the target gene, where the duplex region comprises a  
XX mammalian miRNA target region i.e. a non-coding microRNA (miRNA) that  
XX regulates mRNA at a post-transcriptional level. The present invention  
XX describes a method for controlling ontogenesis of a mammal, function of a  
XX mammalian cell, differentiation of a mammalian cell or viability of a  
XX mammalian cell in the post-transcriptional phase, which comprises  
XX introducing a plasmid vector comprising a promoter and nucleic acid  
XX molecule expressing an miRNA or siRNA silencing precursor to the miRNA.  
XX Accordingly, it provides a cell therapy method for treating cancer,  
XX immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis,  
XX Parkinson's disease, or Alzheimer's disease) or an inflammatory disease  
XX by introducing into the cell the miRNA, siRNA silencing precursor to the  
XX miRNA or the plasmid vector. As such, they can be developed into  
XX pharmaceutical compositions that exhibit cytostatic, immunosuppressive,  
XX nootropic, neuroprotective and antiinflammatory activities and hence can  
XX be used for immunotherapy. This polynucleotide sequence is a human target  
XX gene whose expression is modulated by miRNAs of the invention.  
XX Sequence 3421 BP; 852 A; 859 C; 805 G; 905 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 13; Length 3421;  
Best Local Similarity 100.0%; Pred. No. 0.092;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCCTTGGTTGGGCAACACAT 20  
DB 1926 GCCTTGGTTGGGCAACACAT 1907  
RESULT 11  
ABS73280/c  
ID ABS73280 standard; DNA; 3517 BP.  
XX AC ABS73280;

```
DT 04-DEC-2002 (first entry)
DE DNA encoding human translocation (2; 13) (q35; q14) protein.
DE
XX Chromosome aberration; oncogenic fusion protein; cancer;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
XX
OS Homo sapiens.
XX
XX WO200269900-A2.
XX
XX 12-SEP-2002.
XX
XX 01-MAR-2002; 2002WO-US006518.
XX
XX 01-MAR-2001; 2001US-0272751P.
XX
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX
XX Fritz LC, Burrows FJ;
XX
XX WPI; 2002-698710/75.
XX
XX P-PSDB; ABG95079.
XX
XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90.
XX
XX Disclosure; Page 234-235; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock protein
XX (HSP)-90, or selectively treating cells expressing (II) involving
XX administering HSP90-inhibitor. The method is useful for treating
XX genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This represents the DNA sequence of a chromosome aberration
XX
XX Sequence 3517 BP; 962 A; 841 C; 756 G; 958 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 6; Length 3517;
XX Best Local Similarity 100.0%; Pred. No. 0.092;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GCTTTGGTTGGGCAACACAT 20
XXXXXXXXXXXXXXXXXXXX
Db 2022 GCTTTGGTTGGGCAACACAT 2003
XXXXXXXXXXXXXXXXXXXX
RESULT 12
ID ADQ03122/c
XX ADQ03122 standard; DNA; 3517 BP.
XX
XX ADQ03122;
```

```
XX 26-AUG-2004 (first entry)
XX
XX PAX3-FKHR fusion gene translocation DNA seqid 2.
XX
XX fusion transcript identification; chromosome abnormality;
XX genetic disorder; degenerative disease; cancer; leukaemia;
XX chronic myelogenous leukaemia; CML; gene rearrangement; PAX3-FKHR;
XX translocation; Alveolar rhabdomyosarcoma; ARMS; ss;
XX expressed sequence tag; EST.
XX
XX Homo sapiens.
XX
XX US2004110227-A1.
XX
XX 10-JUN-2004.
XX
XX 19-MAR-2003; 2003US-00391530.
XX
XX 19-MAR-2002; 2002US-0365076P.
XX
XX (LEVA/) LEVANON E.
XX (TOPO/) TOPORIK A.
XX (AKIV/) AKIVA P.
XX
XX Levanon E, Toporik A, Akiva P;
XX
XX WPI; 2004-532613/51.
XX
XX Identifying putative fusion transcripts, by aligning first database of
XX annotated polynucleotide with database of expressed polynucleotide, and
XX identifying expressed polynucleotide complementary to non-contiguous
XX sequences of first database.
XX
XX Example 9; SEQ ID NO 2; 133pp; English.
XX
XX The invention describes a method of identifying (M1) putative fusion
XX transcripts. The method involves computationally aligning a first
XX database of annotated polynucleotide sequences with a second database of
XX expressed polynucleotide sequences, and identifying in the second
XX database an expressed polynucleotide sequence complementary to at least
XX two non-contiguous sequences (S1) of the first database, where the
XX expressed polynucleotide sequence identified is a putative fusion
XX transcript, and (S1) is chosen from non-homologous polynucleotide
XX sequences mapped to different chromosomes, polynucleotide sequences
XX mapped to different loci of a single chromosome and polynucleotide
XX sequences mapped to a single locus and not being a part of a splice
XX isoform, the expressed polynucleotide sequence identified is a putative
XX fusion transcript. (M1) is useful for identifying putative fusion
XX transcripts, for identifying transition points in fusion transcripts, for
XX identifying polynucleotide sequence associated with a disorder associated
XX with gene rearrangements, for identifying polypeptides resulting from
XX putative fusion events, for detecting nucleic acid sequence chimerism
XX indicative of predisposition for disorders associated with genetic
XX rearrangements, and for identifying putative mutagenic agents. (M1) is
XX useful for identifying gene rearrangements, chromosome abnormalities,
XX which are associated with genetic disorders, agents known to cause
XX degenerative diseases such as cancer e.g., leukaemia, chronic myelogenous
XX leukaemia (CML), and in diagnosis of various diseases related to gene
XX rearrangements. This sequence represents a PAX3-FKHR t(2;13) (q35;q14)
XX translocation polynucleotide associated with Alveolar rhabdomyosarcoma
XX (ARMS).
XX
XX Sequence 3517 BP; 962 A; 841 C; 756 G; 958 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 12; Length 3517;
XX Best Local Similarity 100.0%; Pred. No. 0.092;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GCTTTGGTTGGGCAACACAT 20
XXXXXXXXXXXXXXXXXXXX
Db 2022 GCTTTGGTTGGGCAACACAT 2003
XXXXXXXXXXXXXXXXXXXX
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RESULT 13
ADN97721/c
ID  ADN97721 standard; DNA; 4945 BP.
XX
XX
AC  ADN97721;
XX
XX  01-JUL-2004 (first entry)
XX
XX  Mouse foxhead box O1A sequence.
XX
XX  ss; cytostatic; antidiabetic; foxhead box O1A inhibitor;
KW  forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;
KW  diabetes; H-ras gene; antisense; gene expression.
XX
XX  Mus musculus.
XX
XX  WO2004031350-A2.
XX
XX  15-APR-2004.
XX
XX  25-SEP-2003; 2003WO-US030352.
XX
XX  26-SEP-2002; 2002US-00260203.
XX  (AMGE-) AMGEN INC.
XX  (ISIS-) ISIS PHARM INC.
XX
XX  Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;
XX  WPI; 2004-330164/30.
XX
XX  New compounds, particularly antisense oligonucleotides, targeted to a
PT  nucleic acid molecule encoding forkhead box O1A, useful for treating
PT  cancer, or type 2 diabetes.
XX
XX  Example 15; SEQ ID NO 11; 146pp; English.
XX
XX  The invention relates to a compound 8-80 nucleobases in length targeted
CC  to a nucleic acid molecule encoding forkhead box O1A, where the compound
CC  is at least 70% complementary to a nucleic acid molecule encoding
CC  forkhead box O1A and modulates expression of forkhead box O1A by at least
CC  10%. The compound is useful for treating an animal having a disease or
CC  condition associated with forkhead box O1A, e.g. a hyperproliferative
CC  disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This
CC  sequence corresponds to the mouse foxhead box O1A to which the
CC  oligonucleotides of the invention are targeted.
XX
XX  Sequence 4945 BP; 1148 A; 1303 C; 1209 G; 1285 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 12; Length 4945;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTTTGGTTGGCAACACAT 20
Db 2339 GCTTTGGTTGGCAACACAT 2320

RESULT 14
ADN40657/c
ID  ADN40657 standard; DNA; 4945 BP.
XX
XX
AC  ADN40657;
XX
XX  12-AUG-2004 (first entry)
XX
XX  Mouse forkhead box O1A DNA.
XX
XX  Mouse; forkhead box O1A; gene; ds; antisense oligonucleotide;
KW  phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;
KW  5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;
KW  type 2 diabetes; cytostatic; antidiabetic.
XX
```

```
XX  Mus musculus.
OS
XX
XX  Key Location/Qualifiers
PH  CDS 429..2387
FT  /*tag= a
FT  /product= "Mouse forkhead box O1A"
XX
XX  US2004097459-A1.
XX
XX  20-MAY-2004.
XX
XX  25-SEP-2003; 2003US-00671074.
XX
XX  26-SEP-2002; 2002US-00260203.
XX
XX  (DOBI/) DOBIE K W.
XX  (BHAN/) BHANOT S.
XX  (VENI/) VENIANT-ELLISON M.
XX  (LIND/) LINDBERG R A.
XX  (SHUT/) SHUTTER J R.
XX
XX  Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;
XX  WPI; 2004-389194/36.
XX  P-PSDB; ADN40824.
XX  GENBANK; AJ252157.
XX
XX  New compounds, particularly antisense oligonucleotides, targeted to a
PT  nucleic acid molecule encoding forkhead box O1A, useful for treating
PT  cancer, or type 2 diabetes.
XX
XX  Example 15; SEQ ID NO 11; 80pp; English.
XX
XX  The invention relates to a compound targeted to a nucleic acid molecule
CC  encoding the human forkhead box O1A polypeptide. The compound is an
CC  antisense oligonucleotide that specifically hybridizes with the nucleic
CC  acid and inhibits expression of the polypeptide. The antisense
CC  oligonucleotide comprises at least one modified internucleoside linkage
CC  i.e. a phosphorothioate linkage, at least one modified sugar moiety,
CC  preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified
CC  nucleobase comprising a 5-methylcytosine. The antisense compounds are
CC  useful for modulating the expression of the human forkhead box O1A
CC  polypeptide and in preparation of a composition for treating
CC  hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,
CC  and type 2 diabetes. This sequence represents DNA encoding the mouse
CC  forkhead O1A polypeptide of the invention.
XX
XX  Sequence 4945 BP; 1148 A; 1303 C; 1209 G; 1285 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 12; Length 4945;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTTTGGTTGGCAACACAT 20
Db 2339 GCTTTGGTTGGCAACACAT 2320

RESULT 15
ACF87489/c
ID  ACF87489 standard; DNA; 5722 BP.
XX
XX
AC  ACF87489;
XX
XX  02-JUN-2005 (first entry)
XX
XX  Human SIRS/sepsis diagnostic marker DNA fragment 6349.
XX
XX  Systemic inflammatory response syndrome; SIRS; antibacterial;
KW  immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.
XX
XX  Homo sapiens.
OS
```

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XX WO2004087949-A2.
XX
XX PD
XX PF
XX PP
XX 14-OCT-2004.
XX
XX 31-MAR-2004; 2004WO-EP003419.
XX
XX 02-APR-2003; 2003DE-01015031.
XX
XX 08-AUG-2003; 2003DE-01036511.
XX
XX 02-SEP-2003; 2003DE-01040395.
XX
XX (SIRS-) SIRS LAB GMBH.
XX
XX Russwurm S, Reinhart K, Saluz H, Straube E, Zipfel PF, Deigner H;
XX WPI; 2004-748070/73.
XX
XX In vitro detection of systemic inflammatory response syndrome and related
XX conditions, for e.g. monitoring progression, comprises detecting abnormal
XX expression of disease-related genes.
XX
XX Disclosure; Page; 75pp; German.
XX
XX The invention relates to a novel method for in vitro detection of
XX systemic inflammatory response syndrome (SIRS). The method comprises
XX detecting abnormal expression of disease-related genes, or their
XX associated peptides. The method of the invention demonstrates
XX antibacterial, immunosuppressive and antiinflammatory applications and
XX may be used for early differential diagnosis, monitoring progression,
XX assessing risk, assessing the likely response to treatment and for post
XX mortem diagnosis of systemic inflammatory response syndrome, sepsis and
XX sepsis-like conditions. The recombinant or synthetic nucleic acid
XX sequences of the invention, or derived proteins or peptides, may be
XX useful as calibrants in assays for the specified diseases, for evaluating
XX activity or toxicity in screening for active agents and/or for
XX preparation of agents for treatment or prevention of the specified
XX diseases. The current sequence is that of a human SIRS/sepsis diagnostic
XX marker DNA fragment of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at ftp.wipo.int/pub/published
XX pct sequences. Furthermore, a number of arbitrary SEQ ID NO.s are
XX disclosed within the specification, however, these have not been taken
XX into account during indexing due to inconsistencies in application and
XX format
XX
XX Sequence 5722 BP; 1454 A; 1366 C; 1290 G; 1612 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 13; Length 5722;
XX Best Local Similarity 100.0%; Pred. No. 0.092;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCTTTGGTTGGCAACACAT 20
XX |||||||||||||||||||
XX Db 2305 GCTTTGGTTGGCAACACAT 2286
XX
XX RESULT 16
XX ACF87572/c
XX ID ACF87572 standard; DNA; 5722 BP.
XX
XX AC ACF87572;
XX
XX 02-JUN-2005 (first entry)
XX
XX Human SIRS/sepsis diagnostic marker DNA fragment 6432.
XX
XX Systemic inflammatory response syndrome; SIRS; antibacterial;
XX immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.
XX
XX Homo sapiens.
XX
XX WO2004087949-A2.
XX
XX PN
```

```
PD 14-OCT-2004.
XX
XX 31-MAR-2004; 2004WO-EP003419.
XX
XX 02-APR-2003; 2003DE-01015031.
XX
XX 08-AUG-2003; 2003DE-01036511.
XX
XX 02-SEP-2003; 2003DE-01040395.
XX
XX (SIRS-) SIRS LAB GMBH.
XX
XX Russwurm S, Reinhart K, Saluz H, Straube E, Zipfel PF, Deigner H;
XX WPI; 2004-748070/73.
XX
XX In vitro detection of systemic inflammatory response syndrome and related
XX conditions, for e.g. monitoring progression, comprises detecting abnormal
XX expression of disease-related genes.
XX
XX Disclosure; Page; 75pp; German.
XX
XX The invention relates to a novel method for in vitro detection of
XX systemic inflammatory response syndrome (SIRS). The method comprises
XX detecting abnormal expression of disease-related genes, or their
XX associated peptides. The method of the invention demonstrates
XX antibacterial, immunosuppressive and antiinflammatory applications and
XX may be used for early differential diagnosis, monitoring progression,
XX assessing risk, assessing the likely response to treatment and for post
XX mortem diagnosis of systemic inflammatory response syndrome, sepsis and
XX sepsis-like conditions. The recombinant or synthetic nucleic acid
XX sequences of the invention, or derived proteins or peptides, may be
XX useful as calibrants in assays for the specified diseases, for evaluating
XX activity or toxicity in screening for active agents and/or for
XX preparation of agents for treatment or prevention of the specified
XX diseases. The current sequence is that of a human SIRS/sepsis diagnostic
XX marker DNA fragment of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at ftp.wipo.int/pub/published
XX pct sequences. Furthermore, a number of arbitrary SEQ ID NO.s are
XX disclosed within the specification, however, these have not been taken
XX into account during indexing due to inconsistencies in application and
XX format
XX
XX Sequence 5722 BP; 1454 A; 1366 C; 1290 G; 1612 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 13; Length 5722;
XX Best Local Similarity 100.0%; Pred. No. 0.092;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCTTTGGTTGGCAACACAT 20
XX |||||||||||||||||||
XX Db 2305 GCTTTGGTTGGCAACACAT 2286
XX
XX RESULT 17
XX ABV94143/c
XX ID ABV94143 standard; cDNA; 5723 BP.
XX
XX AC ABV94143;
XX
XX 08-JAN-2003 (first entry)
XX
XX Breast carcinoma related nucleotide sequence SEQ ID NO:134.
XX
XX Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200246467-A2.
XX
XX 13-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-IB002811.
XX
XX PN
```

XX 08-DEC-2000; 2000US-0254090P.  
PR 07-DEC-2001; 2001US-00007926.  
XX (IPSO-) IPSOGEN.  
XX Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;  
FI WPI; 2002-619023/66.  
XX Novel polynucleotide library useful in molecular characterization of a  
PT carcinoma, comprising a pool of polynucleotide sequences or its  
PT subsequences which are either underexpressed or overexpressed in tumor  
PT cells.  
XX Claim 1; Page 198-200; 401pp; English.  
XX The present invention describes a polynucleotide library (I) useful in  
CC the molecular characterisation of a carcinoma, comprising a pool of  
CC polynucleotides or its subsequences which are either underexpressed or  
CC overexpressed in tumour cells, and correspond to any of the  
CC polynucleotide sequences chosen from the 468 sequences given in ABV94010  
CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for  
CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting  
CC (MI) differentially expressed polynucleotide sequences which are  
CC correlated with a cancer, involves obtaining a polynucleotide sample from  
CC a patient, and reacting the polynucleotide sample obtained with a probe  
CC immobilised on a solid support, where the probe comprises any combination  
CC of the polynucleotide sequences of (I) or its expression products encoded  
CC by polynucleotide sequences of (I), and detecting the reaction product.  
CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)  
CC is useful in molecular characterisation of a carcinoma. (I) and (II) are  
CC useful for the prognosis or diagnostic of tumour, in differentiating a  
CC normal cell from a cancer cell, detecting a hormone sensitive tumour  
CC cell, differentiating a tumour with lymph nodes from a tumour without  
CC lymph nodes, differentiating antitumor agents from a tumour without  
CC antitumor agents, differentiating antitumor agents from a tumour without  
CC antitumor agents, and classifying good and poor prognosis  
CC primary breast tumours. (I) is useful for large-scale molecular  
CC characterisation of breast cancer that help in prediction, prognosis and  
CC cancer treatment, and for detecting differentially expressed genes that  
CC correlated with a cancer  
XX  
SQ Sequence 5723 BP; 1454 A; 1366 C; 1291 G; 1612 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 5723;  
Best Local Similarity 100.0%; Pred. No. 0.092;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCTTTGGTTGGGCAACACAT 20  
Db 2305 GCTTTGGTTGGGCAACACAT 2286  
RESULT 18  
ADN06031/c  
ID ADN06031 standard; cDNA; 5723 BP.  
AC ADN06031;  
XX 01-JUL-2004 (first entry)  
XX Antipsoriatic cDNA sequence #1254.  
DE ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO2004028479-A2.  
XX 08-APR-2004.  
XX 25-SEP-2003; 2003WO-US030907.  
XX

PR 25-SEP-2002; 2002US-0414006P.  
XX (GETH ) GENENTECH INC.  
XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
FI Wu TD;  
XX WPI; 2004-305105/28.  
DR P-PSDB; ADN06032.  
XX New PRO nucleic acid or polypeptide, useful for preparing a  
PT pharmaceutical composition for diagnosing or treating psoriasis in a  
PT mammal.  
XX Claim 1; SEQ ID NO 2426; 3069pp; English.  
XX The invention relates to novel polynucleotide and polypeptides for  
CC treating psoriasis or a sequence having at least 80% identity to the  
CC above sequences. The nucleic acid is useful for preparing a composition  
CC for diagnosing or treating psoriasis in a mammal. This sequence  
CC corresponds to one of the polynucleotides of the invention.  
XX SQ Sequence 5723 BP; 1454 A; 1366 C; 1291 G; 1612 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 5723;  
Best Local Similarity 100.0%; Pred. No. 0.092;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCTTTGGTTGGGCAACACAT 20  
Db 2305 GCTTTGGTTGGGCAACACAT 2286  
RESULT 19  
ADN97714/c  
ID ADN97714 standard; DNA; 5723 BP.  
XX ADN97714;  
XX 01-JUL-2004 (first entry)  
XX Human foxhead box O1a sequence.  
DE ss; cytostatic; antidiabetic; foxhead box O1a inhibitor;  
XX forkhead box O1a; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
XX diabetes; H-ras gene; antisense; gene expression.  
XX Homo sapiens.  
OS WO2004031350-A2.  
XX 15-APR-2004.  
XX 25-SEP-2003; 2003WO-US030352.  
XX 26-SEP-2002; 2002US-00260203.  
XX (AMGE-) AMGEN INC.  
XX (ISIS-) ISIS PHARM INC.  
XX Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
FI WPI; 2004-330164/30.  
XX New compounds, particularly antisense oligonucleotides, targeted to a  
PT nucleic acid molecule encoding forkhead box O1a, useful for treating  
PT cancer, or type 2 diabetes.  
XX Example 15; SEQ ID NO 4; 146pp; English.  
XX The invention relates to a compound 8-80 nucleobases in length targeted  
CC to a nucleic acid molecule encoding forkhead box O1a, where the compound  
CC is at least 70% complementary to a nucleic acid molecule encoding

CC forkhead box O1A and modulates expression of forkhead box O1A by at least  
CC 10%. The compound is useful for treating an animal having a disease or  
CC condition associated with forkhead box O1A, e.g. a hyperproliferative  
CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This  
CC sequence corresponds to the human forkhead box O1A to which the  
CC oligonucleotides of the invention are targeted.  
XX

SQ Sequence 5723 BP; 1454 A; 1366 C; 1291 G; 1612 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 5723;  
Best Local Similarity 100.0%; Pred. No. 0.092;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGGCAACACAT 20  
|||  
Db 2305 GCTTTGGTTGGGCAACACAT 2286

## RESULT 20

ADN40650/c

ID ADN40650 standard; DNA; 5723 BP.

XX AC ADN40650;

XX DT 12-AUG-2004 (first entry)

XX DE Human forkhead box O1A DNA.

XX KW Human; forkhead box O1A; gene; ds; antisense oligonucleotide;

XX KW phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;

XX KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;

XX KW type 2 diabetes; cytostatic; antidiabetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 386..2353

XX FT /\*tag= a

XX FT /product= "Human forkhead box O1A"

XX PN US2004097459-A1.

XX PD 20-MAY-2004.

XX PF 25-SEP-2003; 2003US-00671074.

XX PR 26-SEP-2002; 2002US-00260203.

XX PA (DOR/) DOBIE K W.

XX PA (BHAN/) BHANOT S.

XX PA (VENI/) VENIANT-ELLISON M.

XX PA (LIND/) LINDBERG R A.

XX PA (SHUT/) SHUTTER J R.

XX PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;

XX DR WPI; 2004-389194/36.

XX DR P-PSDB; ADN40823.

XX DR GENBANK; NM\_002015.

XX PT New compounds, particularly antisense oligonucleotides, targeted to a  
XX nucleic acid molecule encoding forkhead box O1A, useful for treating  
XX cancer, or type 2 diabetes.

PS Example 15; SEQ ID NO 4; 80pp; English.

XX CC The invention relates to a compound targeted to a nucleic acid molecule  
XX encoding the human forkhead box O1A polypeptide. The compound is an  
XX antisense oligonucleotide that specifically hybridises with the nucleic  
XX acid and inhibits expression of the polypeptide. The antisense  
XX oligonucleotide comprises at least one modified internucleoside linkage  
XX i.e. a phosphorothioate linkage, at least one modified sugar moiety,  
XX preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified

CC nucleobase comprising a 5-methylcytosine. The antisense compounds are  
CC useful for modulating the expression of the human forkhead box O1A  
CC polypeptide and in preparation of a composition for treating  
CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,  
CC and type 2 diabetes. This sequence represents DNA encoding the human  
CC forkhead O1A polypeptide of the invention.  
XX

SQ Sequence 5723 BP; 1454 A; 1366 C; 1291 G; 1612 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 5723;  
Best Local Similarity 100.0%; Pred. No. 0.092;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGGCAACACAT 20  
|||  
Db 2305 GCTTTGGTTGGGCAACACAT 2286

## RESULT 21

ACN39628/c

ID ACN39628 standard; cDNA; 5723 BP.

XX AC ACN39628;

XX DT 18-NOV-2004 (first entry)

XX DE Tumour-associated antigenic target (TAT) cDNA DNA270254, SEQ ID NO:3896.

XX KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
XX KW tumour; diagnosis; cell proliferative disorder; breast cancer;  
XX KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
XX KW central nervous system cancer; bladder cancer; pancreatic cancer;  
XX KW cervical cancer; melanoma; leukaemia; hybridisation probe;  
XX KW chromosome identification; chromosome mapping; gene mapping;  
XX KW gene therapy; cytostatic; gene; ss.

XX OS Homo sapiens.

XX PN WO2004030615-A2.

XX PD 15-APR-2004.

XX PF 29-SEP-2003; 2003WO-US028547.

XX PR 02-OCT-2002; 2002US-0414971P.

XX PA (GETH ) GENENTECH INC.

XX PI Wu TD, Zhang Z, Zhou Y;

XX DR WPI; 2004-347921/32.

XX DR P-PSDB; ABM81512.

XX PT New tumor-associated antigenic target polypeptides and nucleic acids,  
XX useful in preparing a medicament for treating or detecting a  
XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
XX prostate cancer or tumor.

PS Claim 1; SEQ ID NO 3896; 7273pp; English.

XX CC The invention relates to human tumour-associated antigenic target (TAT)  
XX polypeptides, and their related nucleic acids. The TAT polypeptides are  
XX overexpressed in cancer tissues compared to normal tissues, and may thus  
XX serve as effective targets for the diagnosis and treatment of cancer in  
XX mammals. The invention also relates to nucleic acid and polypeptide  
XX sequences at least 80% identical to the TAT nucleic acids and  
XX polypeptides; expression vectors and host cells comprising a TAT nucleic  
XX acid; an antibody specific for a TAT polypeptide; a peptide or organic  
XX molecule which binds to a TAT polypeptide; fusion proteins comprising a  
XX TAT polypeptide; and methods and compositions for the treatment or  
XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
XX antibodies, antagonists, binding molecules and compositions are useful  
XX for diagnosing or treating a cell proliferative disorder associated with



CC increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence CC represents a TAT nucleic acid of the invention

XX SQ Sequence 5723 BP; 1454 A; 1366 C; 1291 G; 1612 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 5723;  
Best Local Similarity 100.0%; Pred. No. 0.092;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAACACAT 20  
|||||  
DB 2305 GCTTTGGTTGGCAACACAT 2286

RESULT 22

ADY14881/c

ID ADY14881 standard; DNA; 5723 BP.

XX AC ADY14881;

XX DT 05-MAY-2005 (first entry)

XX DE DNA encoding a PRO polypeptide, SEQ ID NO 687.

XX KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
XX KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
XX KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;  
XX KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;  
XX KW Antiallergic; ds; gene; diagnosis.

XX OS Homo sapiens.

XX PN WO2005016962-A2.

XX PD 24-FEB-2005.

XX PF 11-AUG-2004; 2004WO-US026249.

XX PR 11-AUG-2003; 2003US-0493546P.

XX PA (GETH ) GENENTECH INC.

XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX DR WPI; 2005-182330/19.

XX PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX PS Claim 1; SEQ ID NO 687; 158pp; English.

XX CC The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO polypeptide.

XX SQ Sequence 5723 BP; 1454 A; 1366 C; 1291 G; 1612 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 5723;

Best Local Similarity 100.0%; Pred. No. 0.092;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAACACAT 20  
|||||  
DB 2305 GCTTTGGTTGGCAACACAT 2286

RESULT 23

ADF81591/c

ID ADF81591 standard; DNA; 5769 BP.

XX AC ADF81591;

XX DT 26-FEB-2004 (first entry)

XX DE Leukaemia-related DNA sequence #2147.

XX KW Cytostatic; Gene therapy; leukaemia; ss.

XX OS Unidentified.

XX PN WO2003039443-A2.

XX PD 15-MAY-2003.

XX PF 04-NOV-2002; 2002WO-EP012303.

XX PR 05-NOV-2001; 2001EP-00126244.

XX PR 30-APR-2002; 2002EP-00009758.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PA (UYLU-) UNIV LUDWIG MAXIMILIANS.

XX PA (HAPE/) HAPERLACH T.

XX PA (SCHO/) SCHOCH C.

XX PA (KERN/) KERN W.

XX PI Haferlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;  
XX PI Ellis R, Brors B, Mergenthaler S;

XX DR WPI; 2003-505037/47.

XX PT Determining the subtype of leukemia cells and whether a patient sample contains leukemia cells or other cells, useful for treating leukemia, comprises determining the expression profile of a group of markers in a patient sample.

XX PS Disclosure; SEQ ID NO 2147; 2938pp; English.

XX CC The present invention relates to a method (M1) for determining the subtype of leukaemia cells and whether a patient sample contains leukaemia cells. The method comprises determining the expression profile of a group of markers in a patient sample. The method is useful for determining the presence of leukaemia cells, its types or subtypes, and for the preparation of a medicament for treating leukaemia.

XX SQ Sequence 5769 BP; 1485 A; 1367 C; 1291 G; 1613 T; 0 U; 13 Other;

Query Match 100.0%; Score 20; DB 10; Length 5769;

Best Local Similarity 100.0%; Pred. No. 0.092;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAACACAT 20  
|||||  
DB 2305 GCTTTGGTTGGCAACACAT 2286

RESULT 24

AAS85053/c

ID AAS85053 standard; cDNA; 5833 BP.

XX AC AAS85053;

XX DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #20857.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

```
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSB-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG20866.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX Claim 1; SEQ ID NO 20857; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (II) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 5833 BP; 1482 A; 1383 C; 1331 G; 1637 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 5; Length 5833;
XX Best Local Similarity 100.0%; Pred. No. 0.092;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCTTTGGTTGGGCACACAT 20
XX
XX Db 2357 GCTTTGGTTGGGCACACAT 2338
XX
XX RESULT 25
XX ADN97750
XX ID ADN97750 standard; DNA; 20 BP.
XX
XX AC ADN97750;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Human foxhead box O1A sequence inhibitory oligo #23.
XX
XX ss; cytosstatic; antidiabetic; foxhead box O1A inhibitor;
XX KW foxhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;
XX KW diabetes; H-ras gene; antisense; gene expression; primer.
XX
```

```
OS Synthetic.
XX Key Location/Qualifiers
XX misc_difference 1..20
XX /*tag= b
XX /note= "sugar phosphate internucleotide linkages in the
XX backbone are replaced with a phosphorothioate
XX internucleotide linkages"
XX modified_base 1..20
XX /*tag= c
XX /mod_base= OTHER
XX /note= "all C are 5'-methylcytidines"
XX modified_base 1..5
XX /*tag= a
XX /mod_base= OTHER
XX /note= "nucleotides are 2'-methoxyethyl-nucleotides"
XX modified_base 16..20
XX /*tag= d
XX /mod_base= OTHER
XX /note= "nucleotides are 2'-methoxyethyl-nucleotides"
XX WO2004031350-A2.
XX
XX 15-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030352.
XX
XX 26-SEP-2002; 2002US-00260203.
XX (AMGE-) AMGEN INC.
XX (ISIS-) ISIS PHARM INC.
XX
XX Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;
XX WPI; 2004-330164/30.
XX
XX New compounds, particularly antisense oligonucleotides, targeted to a
XX nucleic acid molecule encoding forkhead box O1A, useful for treating
XX cancer, or type 2 diabetes.
XX
XX Claim 14; SEQ ID NO 40; 146pp; English.
XX
XX The invention relates to a compound 8-80 nucleobases in length targeted
XX to a nucleic acid molecule encoding forkhead box O1A, where the compound
XX is at least 70% complementary to a nucleic acid molecule encoding
XX forkhead box O1A and modulates expression of forkhead box O1A by at least
XX 10%. The compound is useful for treating an animal having a disease or
XX condition associated with forkhead box O1A, e.g. a hyperproliferative
XX disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This
XX sequence corresponds to an oligonucleotide targeted to the human foxhead
XX box O1A genes in order to inhibit gene expression.
XX
XX Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 95.0%; Score 19; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 0.37;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 CTTTGGTTGGGCACACAT 20
XX
XX Db 1 CTTTGGTTGGGCACACAT 19
XX
XX RESULT 26
XX ADN97828/c
XX ID ADN97828 standard; DNA; 20 BP.
XX
XX AC ADN97828;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Human foxhead box O1A gene target sequence #21.
XX
```

ss; cytostatic; antidiabetic; foxhead box O1A inhibitor;  
Kw forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
Kw diabetes; H-ras gene; antisense; gene expression; primer.  
Os Homo sapiens.  
Xx WO2004031350-A2.  
Fn 15-APR-2004.  
Pd 25-SEP-2003; 2003WO-US030352.  
Pp 26-SEP-2002; 2002US-00260203.  
Pr (AMGE-) AMGEN INC.  
Xx (ISIS-) ISIS PHARM INC.  
Pa  
Xx Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
Xx WPI; 2004-330164/30.  
Dr New compounds, particularly antisense oligonucleotides, targeted to a  
Pt nucleic acid molecule encoding forkhead box O1A, useful for treating  
Pt cancer, or type 2 diabetes.  
Xx Example 18; SEQ ID NO 118; 146pp; English.  
Fs The invention relates to a compound 8-80 nucleobases in length targeted  
Xx to a nucleic acid molecule encoding forkhead box O1A, where the compound  
Cc is at least 70% complementary to a nucleic acid molecule encoding  
Cc forkhead box O1A and modulates expression of forkhead box O1A by at least  
Cc 10%. The compound is useful for treating an animal having a disease or  
Cc condition associated with forkhead box O1A, e.g. a hyperproliferative  
Cc disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This  
Cc sequence corresponds to a targeted sequence from the human foxhead box  
Cc O1A gene.  
Xx  
Sq Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 95.0%; Score 19; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.37; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CTTTGGTTGGCAACACAT 20  
Db 20 CTTTGGTTGGCAACACAT 2  
RESULT 27  
ADN40686  
ID ADN40686 standard; DNA; 20 BP.  
Xx  
Xx ADN40686;  
Xx  
Dt 12-AUG-2004 (first entry)  
Xx  
Xx Human forkhead box O1A DNA antisense oligonucleotide #23.  
Xx  
Xx Human; forkhead box O1A; ss; antisense oligonucleotide;  
Kw phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
Kw 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
Xx type 2 diabetes; cytostatic; antidiabetic.  
Xx  
Os Homo sapiens.  
Xx  
Fn US2004097459-A1.  
Xx  
Pd 20-MAY-2004.  
Xx  
Pp 25-SEP-2003; 2003US-00671074.  
Xx  
Pr 26-SEP-2002; 2002US-00260203.  
Xx

Pa (DOBI/) DOBIE K W.  
Pa (BHAN/) BHANOT S.  
Pa (VENI/) VENIANT-ELLISON M.  
Pa (LIND/) LINDBERG R A.  
Pa (SHUT/) SHUTTER J R.  
Xx  
Xx Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
Xx WPI; 2004-389194/36.  
Dr New compounds, particularly antisense oligonucleotides, targeted to a  
Pt nucleic acid molecule encoding forkhead box O1A, useful for treating  
Pt cancer, or type 2 diabetes.  
Xx Claim 14; SEQ ID NO 40; 80pp; English.  
Fs The invention relates to a compound targeted to a nucleic acid molecule  
Xx encoding the human forkhead box O1A polypeptide. The compound is an  
Cc antisense oligonucleotide that specifically hybridizes with the nucleic  
Cc acid and inhibits expression of the polypeptide. The antisense  
Cc oligonucleotide comprises at least one modified internucleoside linkage  
Cc i.e. a phosphorothioate linkage, at least one modified sugar moiety,  
Cc preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified  
Cc nucleobase comprising a 5-methylcytosine. The antisense compounds are  
Cc useful for modulating the expression of the human forkhead box O1A  
Cc polypeptide and in preparation of a composition for treating  
Cc hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,  
Cc and type 2 diabetes. This sequence represents an antisense  
Cc oligonucleotide targeted to DNA encoding the human forkhead O1A  
Cc polypeptide of the invention.  
Xx  
Sq Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 U; 0 Other;  
Query Match 95.0%; Score 19; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.37; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CTTTGGTTGGCAACACAT 20  
Db 1 CTTTGGTTGGCAACACAT 19  
RESULT 28  
ADN40764/c  
ID ADN40764 standard; DNA; 20 BP.  
Xx  
Xx ADN40764;  
Xx  
Dt 12-AUG-2004 (first entry)  
Xx  
Xx Human forkhead box O1A DNA antisense oligonucleotide target region #21.  
Xx  
Xx Human; forkhead box O1A; ss; antisense oligonucleotide;  
Kw phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
Kw 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
Xx type 2 diabetes; cytostatic; antidiabetic.  
Xx  
Os Homo sapiens.  
Xx  
Fn US2004097459-A1.  
Xx  
Pd 20-MAY-2004.  
Xx  
Pp 25-SEP-2003; 2003US-00671074.  
Xx  
Pr 26-SEP-2002; 2002US-00260203.  
Xx  
Pa (DOBI/) DOBIE K W.  
Pa (BHAN/) BHANOT S.  
Pa (VENI/) VENIANT-ELLISON M.  
Pa (LIND/) LINDBERG R A.  
Pa (SHUT/) SHUTTER J R.  
Xx

```

PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;
XX WPI; 2004-389194/36.
DR
XX
XX New compounds, particularly antisense oligonucleotides, targeted to a
PT nucleic acid molecule encoding forkhead box O1A, useful for treating
PT cancer, or type 2 diabetes.
XX
XX Example 18; SEQ ID NO 118; 80pp; English.
XX
XX The invention relates to a compound targeted to a nucleic acid molecule
CC encoding the human forkhead box O1A polypeptide. The compound is an
CC antisense oligonucleotide that specifically hybridizes with the nucleic
CC acid and inhibits expression of the polypeptide. The antisense
CC oligonucleotide comprises at least one modified internucleoside linkage
CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,
CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified
CC nucleobase comprising a 5-methylcytosine. The antisense compounds are
CC useful for modulating the expression of the human forkhead box O1A
CC polypeptide and in preparation of a composition for treating
CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,
CC and type 2 diabetes. This sequence represents a human forkhead O1A DNA
CC antisense oligonucleotide target region of the invention.
XX
XX Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 95.0%; Score 19; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTTTGGTGGGCAACACAT 20
DB 20 CTTTGGTGGGCAACACAT 2
RESULT 29
ABZ16434/c
ID ABZ16434 standard; DNA; 2000 BP.
XX
XX ABZ16434;
AC
XX
XX 21-JAN-2003 (first entry)
DT
XX
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 4239.
DE
XX
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
KW
XX
XX Arabidopsis thaliana.
OS
XX
XX WO200216655-A2.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 24-AUG-2001; 2001WO-US026685.
PP
XX
XX 24-AUG-2000; 2000US-0227866P.
PR
XX
XX 26-JAN-2001; 2001US-0264647P.
PR
XX
XX 22-JUN-2001; 2001US-0300111P.
XX
XX (SCRI ) SCRIPPS RES INST.
PA
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
XX
XX Harper JF, Kreps J, Wang X, Zhu T;
PI
XX
XX WPI; 2002-304127/34.
DR
XX
XX Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
PT
XX
XX Claim 144; SEQ ID NO 4239; 577pp + Sequence Listing; English.
PS
XX
XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid

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CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: the sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
XX Sequence 2000 BP; 657 A; 326 C; 263 G; 754 T; 0 U; 0 Other;
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DB 327 GCTTTGGTGGGCAACA 311
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ID ADN97751 standard; DNA; 20 BP.
XX
XX ADN97751;
AC
XX
XX 01-JUL-2004 (first entry)
DT
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XX Human foxhead box O1A sequence inhibitory oligo #24.
DE
XX
XX ss; cytostatic; antidiabetic; foxhead box O1A inhibitor;
KW forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;
KW diabetes; H-ras gene; antisense; gene expression; primer.
XX
XX Synthetic.
OS
XX
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FT /*tag= c
FT /mod_base= OTHER
FT /note= "all C are 5'-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "nucleotides are 2'-methoxyethyl-nucleotides"
FT modified_base 16..20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "nucleotides are 2'-methoxyethyl-nucleotides"
XX
XX WO2004031350-A2.
XX
XX 15-APR-2004.
PD
XX
XX 25-SEP-2003; 2003WO-US030352.
PP
XX
XX 26-SEP-2002; 2002US-00260203.
PR
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;
PI
XX
XX WPI; 2004-330164/30.
XX
XX New compounds, particularly antisense oligonucleotides, targeted to a

```

PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
PT cancer, or type 2 diabetes.  
PS Claim 14; SEQ ID NO 41; 146pp; English.  
XX  
XX The invention relates to a compound 8-80 nucleobases in length targeted  
CC to a nucleic acid molecule encoding forkhead box O1A, where the compound  
CC is at least 70% complementary to a nucleic acid molecule encoding  
CC forkhead box O1A and modulates expression of forkhead box O1A by at least  
CC 10%. The compound is useful for treating an animal having a disease or  
CC condition associated with forkhead box O1A, e.g. a hyperproliferative  
CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This  
CC sequence corresponds to an oligonucleotide targeted to the human forkhead  
CC box O1A genes in order to inhibit gene expression.  
XX  
SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
  
Query Match 80.0%; Score 16; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 5 GCTTTGGTTGGGCAAC 20  
  
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XX  
XX AC ADN97829;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Human forkhead box O1A gene target sequence #22.  
XX  
XX ss; cytostatic; antidiabetic; forkhead box O1A inhibitor;  
KW forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
KW diabetes; H-ras gene; antisense; gene expression; primer.  
XX  
XX Homo sapiens.  
OS  
XX WO2004031350-A2.  
FN  
XX  
XX 15-APR-2004.  
PD  
XX  
XX 25-SEP-2003; 2003WO-US030352.  
PF  
XX  
XX 26-SEP-2002; 2002US-00260203.  
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XX  
XX (AMGE-) AMGEN INC.  
PA  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX  
PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
XX  
XX WPI; 2004-330164/30.  
DR  
XX  
XX New compounds, particularly antisense oligonucleotides, targeted to a  
PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
PT cancer, or type 2 diabetes.  
XX  
XX Example 18; SEQ ID NO 119; 146pp; English.  
PS  
XX  
XX The invention relates to a compound 8-80 nucleobases in length targeted  
CC to a nucleic acid molecule encoding forkhead box O1A, where the compound  
CC is at least 70% complementary to a nucleic acid molecule encoding  
CC forkhead box O1A and modulates expression of forkhead box O1A by at least  
CC 10%. The compound is useful for treating an animal having a disease or  
CC condition associated with forkhead box O1A, e.g. a hyperproliferative  
CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This  
CC sequence corresponds to a targeted sequence from the human forkhead box  
CC O1A gene.  
XX

SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
  
Query Match 80.0%; Score 16; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GCTTTGGTTGGGCAAC 16  
Db 16 GCTTTGGTTGGGCAAC 1  
  
RESULT 32  
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ID ADN40687 standard; DNA; 20 BP.  
XX  
XX AC ADN40687;  
XX  
XX 12-AUG-2004 (first entry)  
DT  
XX  
XX Human forkhead box O1A DNA antisense oligonucleotide #24.  
DE  
XX  
XX Human; forkhead box O1A; ss; antisense oligonucleotide;  
KW phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
KW type 2 diabetes; cytostatic; antidiabetic.  
XX  
XX Homo sapiens.  
OS  
XX US2004097459-A1.  
FN  
XX 20-MAY-2004.  
PD  
XX  
XX 25-SEP-2003; 2003US-00671074.  
PF  
XX  
XX 26-SEP-2002; 2002US-00260203.  
PR  
XX  
XX (DOBI/) DOBIE K W.  
PA (BHAN/) BHANOT S.  
PA (VENI/) VENIANT-ELLISON M.  
PA (LIND/) LINDBERG R A.  
PA (SHUT/) SHUTTER J R.  
XX  
XX Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
PI  
XX  
XX WPI; 2004-389194/36.  
DR  
XX  
XX New compounds, particularly antisense oligonucleotides, targeted to a  
PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
PT cancer, or type 2 diabetes.  
PF  
XX  
XX Claim 14; SEQ ID NO 41; 80pp; English.  
PS  
XX  
XX The invention relates to a compound targeted to a nucleic acid molecule  
CC encoding the human forkhead box O1A polypeptide. The compound is an  
CC antisense oligonucleotide that specifically hybridizes with the nucleic  
CC acid and inhibits expression of the polypeptide. The antisense  
CC oligonucleotide comprises at least one modified internucleoside linkage,  
CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,  
CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified  
CC nucleobase comprising a 5-methylcytosine. The antisense compounds are  
CC useful for modulating the expression of the human forkhead box O1A  
CC polypeptide and in preparation of a composition for treating  
CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,  
CC and type 2 diabetes. This sequence represents an antisense  
CC oligonucleotide targeted to DNA encoding the human forkhead O1A  
CC polypeptide of the invention.  
XX  
SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
  
Query Match 80.0%; Score 16; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 GCTTTGGTTGGCAAC 20

RESULT 33
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ID ADN40765 standard; DNA; 20 BP.
XX AC
XX ADN40765;
XX XX
DT 12-AUG-2004 (first entry)
XX XX
DE Human forkhead box O1A DNA antisense oligonucleotide target region #22.
XX KW Human; forkhead box O1A; ss; antisense oligonucleotide;
KW phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;
KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;
KW type 2 diabetes; cytostatic; antidiabetic.
XX OS Homo sapiens.
XX PN US2004097459-A1.
XX PD 20-MAY-2004.
XX PF 25-SEP-2003; 2003US-00671074.
XX PR 26-SEP-2002; 2002US-00260203.
XX PA (DOI/) DOBIE K W.
XX PA (BHANI/) BHANOT S.
XX PA (VENI/) VENIANT-ELLISON M.
XX PA (LIND/) LINDBERG R A.
XX PA (SHUT/) SHUTTER J R.
XX PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;
XX WPI; 2004-389194/36.
XX DR
XX PT New compounds, particularly antisense oligonucleotides, targeted to a
XX PT nucleic acid molecule encoding forkhead box O1A, useful for treating
XX PT cancer, or type 2 diabetes.
XX PS Example 18; SEQ ID NO 119; 80pp; English.
XX CC The invention relates to a compound targeted to a nucleic acid molecule
XX CC encoding the human forkhead box O1A polypeptide. The compound is an
XX CC antisense oligonucleotide that specifically hybridizes with the nucleic
XX CC acid and inhibits expression of the polypeptide. The antisense
XX CC oligonucleotide comprises at least one modified internucleoside linkage
XX CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,
XX CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified
XX CC nucleobase comprising a 5-methylcytosine. The antisense compounds are
XX CC useful for modulating the expression of the human forkhead box O1A
XX CC polypeptide and in preparation of a composition for treating
XX CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,
XX CC and type 2 diabetes. This sequence represents a human forkhead O1A DNA
XX CC antisense oligonucleotide target region of the invention.
XX SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAAC 16
Db 16 GCTTTGGTTGGCAAC 1

RESULT 34
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.
XX Disclosure; SEQ ID NO 7739; 1297pp + Sequence Listing; English.
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention
XX SQ Sequence 4106 BP; 1278 A; 669 C; 703 G; 1456 T; 0 U; 0 Other;
Query Match 80.0%; Score 16; DB 4; Length 4106;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 TTGGTTGGGCACACA 19
Db 1936 TTGGTTGGGCACACA 1951
RESULT 35
ABL97944
ID ABL97944 standard; DNA; 4106 BP.
XX AC ABL97944;
XX 21-JUN-2002 (first entry)
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2596.
XX Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disease; infection; cytostatic; gene; ds.
OS Homo sapiens.
XX WO200155317-A2.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US001329.
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
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PR 16-MAR-2000; 2000US-0189874P.
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PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
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PR 07-JUL-2000; 2000US-0216880P.  
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 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225213P.  
 PR 14-AUG-2000; 2000US-0225214P.  
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 PR 08-NOV-2000; 2000US-0246524P.  
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 PR 08-NOV-2000; 2000US-0246527P.  
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 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246610P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249208P.  
 PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
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 PR 17-NOV-2000; 2000US-0249213P.  
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 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.  
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 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 11-DEC-2000; 2000US-0251990P.  
 PR 05-JAN-2001; 2000US-0254097P.  
 PR 05-JAN-2001; 2000US-0259678P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Rosen CA, Barash SC, Ruben SM;  
 PI WPI; 2001-483232/52.  
 DR Nucleic acids encoding 973 human testicular antigen polypeptides, useful  
 PT for preventing, diagnosing and/or treating testicular cancer.  
 XX Disclosure; SEQ ID NO 2596; 766pp; English.  
 XX The present invention provides the protein and coding sequences of 973  
 CC human testicular antigens, and fragments of their genomic sequences. The  
 CC sequences can be used in the treatment of cardiovascular, immune, and  
 CC reproductive system, immune, respiratory, neurological and  
 CC gastrointestinal disorders, infections, and particularly cancer,  
 CC especially testicular cancers. The present sequence is a DNA encoding a  
 CC protein fragment of the invention  
 XX Sequence 4106 BP; 1278 A; 669 C; 703 G; 1456 T; 0 U; 0 Other;  
 SQ

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Query Match      80.0%; Score 16; DB 4; Length 4106;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 TTGGTTGGGCAACACA 19
Db      1936 TTGGTTGGGCAACACA 1951

RESULT 36
ADL13962/C
ID ADL13962 standard; DNA; 160198 BP.
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XX
AC ADL13962;
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DT 06-MAY-2004 (first entry)
XX
DE Osteoarthritis-associated polymorphic nucleotide #494.
XX
XX ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
XX joint space narrowing; osteophyte development; joint pain;
XX osteoarthritis; SNP; single nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO2003054166-A2.
XX
XX 03-JUL-2003.
XX
XX 19-DEC-2002; 2002WO-US041225.
XX
XX 20-DEC-2001; 2001US-0342603P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Jones KA, Schafer A;
XX
XX WPI; 2003-559141/52.
XX
XX Determining susceptibility of an individual to joint space narrowing,
XX osteophyte development and/or joint pain comprises identifying whether
XX the individual has at least one polymorphism in a polynucleotide encoding
XX a protein.
XX
XX Disclosure; SEQ ID NO 494; 297pp; English.
XX
XX The invention relates to a method of determining susceptibility of an
XX individual to joint space narrowing and/or osteophyte development and/or
XX joint pain comprising identifying whether the individual has at least one
XX polymorphism in a polynucleotide encoding at least one of the protein
XX listed in the specification. The methods, composition and agent are
XX useful for modulating the susceptibility of an individual to joint space
XX narrowing and/or osteophyte development and/or joint pain that is
XX associated with a disease, preferably osteoarthritis. The cell line and
XX the non-human animal are useful for screening for an agent for diagnosing
XX osteophyte development and/or joint pain. This sequence corresponds to
XX the polynucleotide encoding a protein listed in the specification. (Note:
XX The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences).
XX
XX SQ Sequence 160198 BP; 48087 A; 32398 C; 32827 G; 46852 T; 0 U; 34 Other;

Query Match      80.0%; Score 16; DB 10; Length 160198;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTTTGGTTGGGCAAC 16
Db      157646 GCTTTGGTTGGGCAAC 157631

RESULT 37
ADL13904/C
ID ADL13904 standard; DNA; 164772 BP.
XX
XX
AC ADL13904;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Osteoarthritis-associated polymorphic nucleotide #436.
XX
XX ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
XX joint space narrowing; osteophyte development; joint pain;
XX osteoarthritis; SNP; single nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO2003054166-A2.
XX
XX 03-JUL-2003.
XX
XX 19-DEC-2002; 2002WO-US041225.
XX
XX 20-DEC-2001; 2001US-0342603P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Jones KA, Schafer A;
XX
XX WPI; 2003-559141/52.
XX
XX Determining susceptibility of an individual to joint space narrowing,
XX osteophyte development and/or joint pain comprises identifying whether
XX the individual has at least one polymorphism in a polynucleotide encoding
XX a protein.
XX
XX Disclosure; SEQ ID NO 436; 297pp; English.
XX
XX The invention relates to a method of determining susceptibility of an
XX individual to joint space narrowing and/or osteophyte development and/or
XX joint pain comprising identifying whether the individual has at least one
XX polymorphism in a polynucleotide encoding at least one of the protein
XX listed in the specification. The methods, composition and agent are
XX useful for modulating the susceptibility of an individual to joint space
XX narrowing and/or osteophyte development and/or joint pain that is
XX associated with a disease, preferably osteoarthritis. The cell line and
XX the non-human animal are useful for screening for an agent for diagnosing
XX osteophyte development and/or joint pain. This sequence corresponds to
XX the polynucleotide encoding a protein listed in the specification. (Note:
XX The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences).
XX
XX SQ Sequence 164772 BP; 50645 A; 32137 C; 31960 G; 50022 T; 0 U; 8 Other;

Query Match      80.0%; Score 16; DB 10; Length 164772;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 TTGGTTGGGCAACACA 19
Db      49632 TTGGTTGGGCAACACA 49617

RESULT 38
ADL88066
ID ADL88066 standard; DNA; 406 BP.
XX
XX
AC ADL88066;
XX
XX
DT 20-MAY-2004 (first entry)
XX
DE DNA up-regulated in murine haematopoietic stem cells cells SeqID 4459.
```

XX gene potential; multi-lineage; cell commitment; haematopoietic stem cell;  
 KW HSC; multipotent progenitor; MPP; common lymphoid progenitor; CLP;  
 KW common myeloid progenitor; CMP; bone marrow stem cell; mouse; murine; ds.  
 XX Mus sp.  
 OS WO2003093445-A2.  
 PN 13-NOV-2003.  
 PD  
 XX  
 XX 05-MAY-2003; 2003WO-US014114.  
 PF 03-MAY-2002; 2002US-0377383P.  
 XX (STOW-) STOWERS INST MEDICAL RES.  
 XX Li L;  
 PI WPI; 2004-022656/02.  
 DR  
 XX Classifying an unknown multi-lineage affiliated gene comprises isolating  
 PT expressed nucleic acid sequences from the discrete cell sub-populations.  
 PT Claim 7; SEQ ID NO 4459; 123pp; English.  
 XX This invention relates to a novel method for predicting gene potential by  
 CC associating nucleic acid sequences of unknown function with particular  
 CC sub-population profiles. Specifically, it refers to classifying an  
 CC unknown multi-lineage affiliated gene by collecting hybridisation data to  
 CC develop a gene expression map, in order to determine the discrete sub-  
 CC population where it is expressed. The present invention describes methods  
 CC for predicting the lineage commitment of genes associated with the self-  
 CC renewing haematopoietic (blood) stem cells (HSCs), as well as the non-  
 CC self renewing multipotent progenitors (MPPs), common lymphoid progenitors  
 CC (CLPs) and common myeloid progenitors (CMPs), which are collectively  
 CC referred to as bone marrow stem cells populations. As such, these methods  
 CC can be used to identify associated multi-lineage affiliated genes and  
 CC hence the underlying molecular mechanisms in physiological haematopoietic  
 CC development. This polynucleotide sequence is DNA associated with a murine  
 CC HSC sub population of cells of the invention.  
 XX SQ Sequence 406 BP; 103 A; 70 C; 94 G; 136 T; 0 U; 3 Other;  
 Query Match 75.0%; Score 15; DB 12; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GGTTGGGCAACACAT 20  
 DB 267 GGTTGGGCAACACAT 281  
 RESULT 39  
 ADL88067  
 ID ADL88067 standard; DNA; 406 BP.  
 XX  
 AC ADL88067;  
 XX  
 XX 20-MAY-2004 (first entry)  
 DT  
 DE DNA up-regulated in murine haematopoietic stem cells SeqID 4460.  
 XX gene potential; multi-lineage; cell commitment; haematopoietic stem cell;  
 KW HSC; multipotent progenitor; MPP; common lymphoid progenitor; CLP;  
 KW common myeloid progenitor; CMP; bone marrow stem cell; mouse; murine; ds.  
 XX Mus sp.  
 OS WO2003093445-A2.  
 PN 13-NOV-2003.  
 PD  
 XX

PF 05-MAY-2003; 2003WO-US014114.  
 XX 03-MAY-2002; 2002US-0377383P.  
 XX (STOW-) STOWERS INST MEDICAL RES.  
 XX Li L;  
 PI WPI; 2004-022656/02.  
 DR  
 XX Classifying an unknown multi-lineage affiliated gene comprises isolating  
 PT expressed nucleic acid sequences from the discrete cell sub-populations.  
 PT Claim 7; SEQ ID NO 4460; 123pp; English.  
 XX This invention relates to a novel method for predicting gene potential by  
 CC associating nucleic acid sequences of unknown function with particular  
 CC sub-population profiles. Specifically, it refers to classifying an  
 CC unknown multi-lineage affiliated gene by collecting hybridisation data to  
 CC develop a gene expression map, in order to determine the discrete sub-  
 CC population where it is expressed. The present invention describes methods  
 CC for predicting the lineage commitment of genes associated with the self-  
 CC renewing haematopoietic (blood) stem cells (HSCs), as well as the non-  
 CC self renewing multipotent progenitors (MPPs), common lymphoid progenitors  
 CC (CLPs) and common myeloid progenitors (CMPs), which are collectively  
 CC referred to as bone marrow stem cells populations. As such, these methods  
 CC can be used to identify associated multi-lineage affiliated genes and  
 CC hence the underlying molecular mechanisms in physiological haematopoietic  
 CC development. This polynucleotide sequence is DNA associated with a murine  
 CC HSC sub population of cells of the invention.  
 XX SQ Sequence 406 BP; 103 A; 70 C; 94 G; 136 T; 0 U; 3 Other;  
 Query Match 75.0%; Score 15; DB 12; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GGTTGGGCAACACAT 20  
 DB 267 GGTTGGGCAACACAT 281  
 RESULT 40  
 ACH45273/c  
 ID ACH45273 standard; cDNA; 498 BP.  
 XX  
 AC ACH45273;  
 XX  
 DT 13-OCT-2003 (first entry)  
 DE Human foetal brain cDNA #5998.  
 XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
 KW genome mapping; biodiversity; genetic disorder.  
 XX Homo sapiens.  
 OS US2003073623-A1.  
 XX 17-APR-2003.  
 PD  
 XX 30-JUL-2001; 2001US-00918995.  
 PF 30-JUL-2001; 2001US-00918995.  
 XX (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
 XX

DR WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful

PT as hybridization probes, as oligomers for PCR, for chromosome and gene

PT mapping, in the recombinant production of protein, or in generating

XX antisense DNA or RNA.

PS Claim 1; SEQ ID NO 32485; 44pp; English.

XX

CC The invention relates to an isolated polynucleotide comprising any one of

CC 38043 cDNA sequences, appearing as ACH1789-ACH50831, whose sequence was

CC determined by the technique of SBH (sequencing by hybridisation). Also

CC included is a purified polypeptide comprising a sequence corresponding to

CC a reading frame of the novel polynucleotide. The nucleic acid sequences

CC are useful in diagnostics as expressed sequence tags (EST) for

CC identifying expressed genes or for physical mapping of the human genome,

CC in forensics, in assessing biodiversity, or in identifying mutations

CC responsible for genetic disorders and other traits. The nucleotide

CC sequences are also useful as hybridisation probes, as oligomers for PCR,

CC for chromosome and gene mapping, in the recombinant production of

CC protein, or in generating antisense DNA or RNA. The purified polypeptide

CC is useful for generating antibodies specific for it. The present sequence

CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data

CC for this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?DocID=20030073623

XX

SQ Sequence 498 BP; 128 A; 139 C; 136 G; 86 T; 0 U; 9 Other;

Query Match 75.0%; Score 15; DB 9; Length 498;

Best Local Similarity 100.0%; Pred. No. 67;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGGCA 15

Db 253 GCTTTGGTTGGGCA 239

RESULT 41

AAK88397

ID AAK88397 standard; cDNA; 574 BP.

XX

AC AAK88397;

XX

DT 05-NOV-2001 (first entry)

XX

DE Human digestive system antigen coding sequence SEQ ID NO: 713.

XX

KW Human; digestive system antigen; gene therapy; cancer; appendicitis;

KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

KW digestive system disorder; Meckel's diverticulum; ss.

XX

OS Homo sapiens.

XX

FN WO200155314-A2.

XX

PD 02-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US001324.

XX

PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226681P.

PR 23-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 12-SEP-2000; 2000US-0232081P.

PR 12-SEP-2000; 2000US-0231968P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.

PR 14-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0248524P.  
PR 08-NOV-2000; 2000US-0248525P.  
PR 08-NOV-2000; 2000US-0248526P.  
PR 08-NOV-2000; 2000US-0248527P.  
PR 08-NOV-2000; 2000US-0248528P.  
PR 08-NOV-2000; 2000US-0248532P.  
PR 08-NOV-2000; 2000US-0248609P.  
PR 08-NOV-2000; 2000US-0248610P.  
PR 08-NOV-2000; 2000US-0248611P.  
PR 17-NOV-2000; 2000US-0248613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
(HUMA-) HUMAN GENOME SCI INC.  
Rosen CA, Barash SC, Ruben SM;  
WPI; 2001-502630/55.  
P-PSDB; AAM92624.  
Polynucleotides encoding digestive system antigens, useful for  
diagnosing, treating, preventing and/or prognosing disorders of the  
digestive system, particularly cancer and cancer metastases.  
Claim 1; SEQ ID NO 713; 986pp; English.  
The present invention provides the protein and coding sequences of a  
number of human digestive system antigens. These can be used in the  
diagnosis, treatment and prevention of digestive system disorders,  
including cancer, Meckel's diverticulum, bacterial or parasitic  
infections, appendicitis, Hirschsprung's disease, chronic colitis or  
ulcerative colitis. The present sequence is a cDNA encoding a digestive  
system antigen of the invention  
Sequence 574 BP; 148 A; 113 C; 137 G; 172 T; 0 U; 4 Other;

Query Match 75.0%; Score 15; DB 4; Length 574;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 TTGTGTTGGCAACA 17  
|||||  
Db 539 TTGTGTTGGCAACA 553  
RESULT 42  
AAS39498  
ID AAS39498 standard; cDNA; 574 BP.  
XX AAS39498;  
XX 17-DEC-2001 (first entry)  
XX cDNA encoding novel human colon associated polypeptide #151.  
KW Human; colon cancer; congenital abnormality; infection; colitis;  
KW inflammatory bowel disease; IBD; neoplastic disorder; gene therapy;  
KW intestinal inflammatory disorder; malabsorption syndrome; gastric;  
KW sigmoid disease; antibacterial; antiviral; antiinflammatory; cytostatic;  
KW ss.  
XX Homo sapiens.  
XX WO200155302-A2.  
XX 02-AUG-2001.  
XX 17-JAN-2001; 2001WO-US001240.  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236328P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.

PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
PI  
XX WPI; 2001-465567/50.  
DR P-PSDB; AAU22618.  
XX  
PT Isolated polypeptide for treating, preventing and/or prognosing  
PT disorders related to the colon including colon cancers and also for  
PT testing and detection e.g. diagnosis.  
XX  
PS Claim 4; SEQ ID NO 161; 562pp; English.  
XX  
CC The present invention relates to the isolation of novel human colon  
CC associated polypeptides (AAU22468-AAU22701), and the cDNA and genomic  
CC sequences encoding for them. The sequences of the invention are useful in  
CC the diagnosis, treatment, prevention and/or prognosis of disorders of the  
CC colon including colon cancer, congenital abnormalities (e.g. atresia and  
CC stenosis), bacterial and viral infections, inflammatory bowel disease  
CC (IBD), neoplastic cell disorders (e.g. polyps and adenomas, intestinal  
CC inflammatory disorders, colitis, colonic inflammation, diarrhoea and  
CC dysentery, malabsorption syndromes (e.g. lactose intolerance), intestinal  
CC obstruction and sigmoid diseases. The polynucleotide sequences of the  
CC invention can also be used in gene therapy. AAS39348-AAS39581 represent  
CC cDNA sequences encoding for the novel human colon associated polypeptides  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 574 BP; 148 A; 113 C; 137 G; 172 T; 0 U; 4 Other;  
Query Match 75.0%; Score 15; DB 5; Length 574;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 TTGTGTTGGGCAACA 17  
|||||  
Db 539 TTGTGTTGGGCAACA 553  
RESULT 43  
ADB32224  
ID ADB32224 standard; cDNA; 574 BP.  
XX  
AC ADB32224;  
XX  
DT 04-DEC-2003 (first entry)  
XX

DE Human novel colon related polypeptide cDNA SEQ ID NO 161.  
XX gene therapy; ss; gene; cancer; liver disorder; hepatitis;  
KW neural disorder; Alzheimer's disease; human; colon.  
XX Homo sapiens.  
OS  
XX  
PN US2003050231-A1.  
XX  
PD 13-MAR-2003.  
XX  
PF  
PP  
XX 17-JAN-2001; 2001US-00764872.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205513P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225475P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226273P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226688P.  
PR 23-AUG-2000; 2000US-0227182P.  
PR 30-AUG-2000; 2000US-0227009P.  
PR 01-SEP-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 13-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 20-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0241826P.  
PR 08-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246533P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 06-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.



PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
XX (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
XX  
XX  
PI Rosen CA, Ruben SM, Barash SC;  
XX  
DR WPI; 2003-625420/59.  
DR P-PSDB; ADB32458.  
XX  
XX New nucleic acid molecule, useful for preparing a medicament for  
PT preventing, treating or ameliorating a medical condition e.g. cancer,  
PT liver disorders or neural disorders.  
XX  
XX Claim 3; SEQ ID NO 161; 216pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule encoding a  
CC polypeptide. The nucleic acid is useful for preparing a medicament for  
CC preventing, treating or ameliorating a medical condition e.g. cancer,  
CC liver disorders such as hepatitis or neural disorders such as Alzheimer's  
CC disease. The present sequence represents a human cDNA encoding a novel  
CC colon related polypeptide. Note: The sequence data for this patent did  
CC not form part of the printed specification but was obtained in electronic  
CC format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030050231.  
XX  
XX Sequence 574 BP; 148 A; 113 C; 137 G; 172 T; 0 U; 4 Other;  
SQ  
Query Match 75.0%; Score 15; DB 9; Length 574;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 TTTGGTTGGGCAACA 17  
Db 539 TTTGGTTGGGCAACA 553  
RESULT 44  
AAS75868/C  
ID AAS75868 standard; cDNA; 1263 BP.  
XX  
AC AAS75868;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #11672.  
XX  
KW Human; chromosome mapping; Gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200175067-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US008631.  
XX  
XX 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI; 2001-639362/73.  
DR  
DR P-PSDB; ABG11681.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
XX Claim 1; SEQ ID NO 11672; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activities. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1263 BP; 403 A; 292 C; 361 G; 207 T; 0 U; 0 Other;  
Query Match 75.0%; Score 15; DB 5; Length 1263;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCTTTGGTTGGGCAA 15  
Db 255 GCTTTGGTTGGGCAA 241  
RESULT 45  
AAV31252  
ID AAV31252 standard; DNA; 1342 BP.  
XX  
XX AAV31252;  
XX  
XX 01-OCT-1998 (first entry)  
XX  
DE E. coli J96 pathogenicity island contig #66.  
XX  
KW PAI; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR;  
KW PAI V; pheV; vaccine; protective immune response; ds.  
XX  
OS Escherichia coli.  
XX  
XX WO9822575-A2.  
XX  
XX 28-MAY-1998.  
XX  
XX 21-NOV-1997; 97WO-US021347.  
XX  
XX 22-NOV-1996; 96US-0031626P.  
PR 14-OCT-1997; 97US-0061953P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX (UYWI-) UNIV WISCONSIN.  
XX  
XX Dillon FJ, Choi GH, Welch RA;  
XX WPI; 1998-312461/27.  
XX  
XX New isolated uropathogenic E. coli nucleotide sequences - used to develop  
PT products for the detection of pathogenic E. coli and to elicit an immune  
PT response to pathogenic E. coli.  
XX

PS Claim 21; Page 167-168; 250pp; English.

XX This sequence represents a E. coli strain J96 contig containing

CC pathogenicity island (PAI) sequences, and represents a nucleic acid

CC molecule of the invention. PAIs are large fragments of DNA which comprise

CC pathogenicity determinants. The sequences of the invention are taken from

CC PAI IV and PAI V. PAI IV is located at approximately 64 min (near pheV)

CC on the E. coli chromosome and is greater than 170 kb. PAI V is located at

CC approximately 94 min (at pheK) on the E. coli chromosome and is

CC approximately 160 kb in size. Antibodies specific to the proteins encoded

CC by the PAI open reading frames of the invention can be used in kits to

CC detect uropathogenic E. coli. The proteins are used in vaccines to elicit

CC a protective immune response in an animal to the uropathogenic E. coli

XX strain J96

SQ Sequence 1342 BP; 368 A; 319 C; 266 G; 381 T; 0 U; 8 Other;

Query Match 75.0%; Score 15; DB 2; Length 1342;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAA 15

|||||

Db 614 GCTTTGGTTGGCAA 628

RESULT 46

ID ADM02861/c

XX ADM02861 standard; cDNA; 1550 BP.

AC ADM02861;

XX 20-MAY-2004 (first entry)

XX Human cDNA of the invention SEQ ID NO:1546.

XX ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.

XX Homo sapiens.

XX EP1347046-A1.

XX 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2003-723558/69.

DR P-PSDB; ADM05304.

XX New polynucleotides and polypeptides are useful in gene therapy, for

PT developing a diagnostic marker or medicines for regulating their

PT expression and activity, or as a target of gene therapy.

XX Claim 1; SEQ ID NO 1546; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded

CC polypeptide. A polynucleotide of the invention may have a use in gene

CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful

CC as a primer for synthesizing the polynucleotide or as a probe for

CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are

CC useful in gene therapy, for developing a diagnostic marker or medicines

CC for regulating their expression and activity, or as a target of gene

CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides

CC are useful as pharmaceutical agents. The present sequence represents a

CC cDNA sequence of the invention.

XX Sequence 1550 BP; 495 A; 332 C; 423 G; 300 T; 0 U; 0 Other;

SQ Query Match 75.0%; Score 15; DB 11; Length 1550;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAA 15

|||||

Db 269 GCTTTGGTTGGCAA 255

RESULT 47

ID ABQ75898 standard; cDNA; 1635 BP.

XX ABQ75898;

XX 17-OCT-2002 (first entry)

XX Human ubiquitin relative protein 46.64 cDNA.

XX Human; ubiquitin relative protein 46.64; tumour; inflammation;

KW immunological disease; haemopathy; human immunodeficiency virus; HIV;

KW gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 55..1329

FT /\*tag= a

FT /product= "ubiquitin relative protein 46.64"

XX CN1339485-A.

XX 13-MAR-2002.

XX 23-AUG-2000; 2000CN-00119708.

XX 23-AUG-2000; 2000CN-00119708.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-464069/50.

DR P-PSDB; ABQ75898.

XX New polypeptide-human ubiquitin protein relative protein 46.64 for

PT treating malignant tumors, inflammations, immunological diseases,

PT hemopathy and human immunodeficiency virus infection.

XX Claim 6; Page 24-25 (disclosure); 33pp; Chinese.

XX The present invention discloses a new kind of polypeptide, human

CC ubiquitin relative protein 46.64, polynucleotides for encoding this

CC polypeptide, and a DNA recombination process to produce the polypeptide.

CC The present invention also discloses the method of applying the

CC polypeptide in treating various diseases, such as malignant tumours,

CC inflammations, immunological diseases, haemopathy and human

CC immunodeficiency virus (HIV) infection. The current sequence represents

CC the human ubiquitin relative protein 46.64 cDNA

XX Sequence 1635 BP; 529 A; 290 C; 344 G; 472 T; 0 U; 0 Other;

SQ Query Match 75.0%; Score 15; DB 6; Length 1635;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCTTGGGCAACACAT 20

|||||

Db 132 GCTTGGGCAACACAT 146

```
RESULT 48
ADF03345
ID ADF03345 standard; DNA; 1701 BP.
XX
XX
AC ADF03345;
XX
DT 12-FEB-2004 (first entry)
XX
XX Bacterial polynucleotide #3630.
XX
XX Proteus mirabilis infection; bacterial infection; antibacterial;
KW immunostimulant; gene; ds.
XX
XX Proteus mirabilis.
OS
XX
XX US6605709-B1.
PN
XX
PD 12-AUG-2003.
XX
XX 05-APR-2000; 2000US-00543681.
PF
XX 09-APR-1999; 99US-0128706P.
PR
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX Breton GL;
PI
XX WPI; 2003-895291/82.
DR
DR P-PSDB; ADF07517.
XX
XX New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.
XX
PS Disclosure; SEQ ID NO 3630; 870pp; English.
XX
XX The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides, methods for producing the polypeptides, a method of
CC generating vaccines for immunising an individual against P. mirabilis, a
CC method for evaluating a compound for the ability to bind a P. mirabilis
CC polypeptide and a method for screening test compounds for anti-bacterial
CC activity. The polypeptides and polynucleotides are useful as molecular
CC targets for diagnosing, preventing and treating pathological conditions
CC resulting from bacterial infection, as reagents for diagnosis of
CC bacterial diseases, as components of antibacterial vaccines, as targets
CC for antibacterial drugs or as bio-control agents for plants. This
CC sequence represents a Proteus mirabilis polynucleotide of the invention.
XX
SQ Sequence 1701 BP; 560 A; 292 C; 326 G; 523 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGTTGGGCAACAC 18
DB 1271 TTGGTTGGGCAACAC 1285

RESULT 49
ACA21214
ID ACA21214 standard; DNA; 2154 BP.
XX
XX ACA21214;
AC
XX
DT 19-JUN-2003 (first entry)
XX
XX Prokaryotic essential gene #2871.
DE
XX
XX Antisense; db; prokaryotic essential gene; cell proliferation;
KW
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KW drug design; gene.
XX
XX Acinetobacter baumannii.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX
XX 06-SEP-2001; 2001US-00948993.
XX
XX 25-OCT-2001; 2001US-0342923P.
XX
XX 08-FEB-2002; 2002US-00072851.
XX
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX
XX P-PSDB; ABUI7344.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 9084; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 2154 BP; 610 A; 460 C; 488 G; 596 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 8; Length 2154;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGGTTGGCAAC 15
DB 860 GCATTGGTTGGCAAC 874
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RESULT 50
ADA32702
ID ADA32702 standard; DNA; 2181 BP.
XX
AC ADA32702;
XX
DT 20-NOV-2003 (first entry)
XX
DE DNA encoding Acinetobacter baumannii protein #3989.
XX
ds, gene; Acinetobacter baumannii; bacterial disease; antibacterial;
KW vaccine; plant biocontrol agent.
XX
OS Acinetobacter baumannii.
XX
PN US6562958-B1.
XX
PD 13-MAY-2003.
XX
PF 04-JUN-1999; 99US-00328352.
XX
PR 09-JUN-1998; 98US-0088701P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton G, Bush D;
XX
WPI; 2003-576092/54.
DR P-PSDB; ADA36828.
XX
New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
PT for diagnosing a bacterial disease, as components of antibacterial
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT plants.
XX
PS Example; SEQ ID NO 3989; 328pp; English.
XX
CC The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC The A. baumannii nucleic acids and polypeptides are useful as reagents
CC for diagnosing a bacterial disease, as components of antibacterial
CC vaccines, as targets for antibacterial drugs, to detect the presence of
CC A. baumannii and other Acinetobacter species in a sample, in screening
CC compounds for the ability to interfere with the A. baumannii life cycle
CC or to inhibit A. baumannii infection, and as biocontrol agents for
CC plants. The present sequence represents DNA encoding an A. baumannii
CC protein.
XX
SQ Sequence 2181 BP; 621 A; 459 C; 492 G; 609 T; 0 U; 0 Other;
Query Match 75.0%; Score 15; DB 9; Length 2181;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTGGTTGGCAA 15
Db 884 GCTTGGTTGGCAA 898
Search completed: May 7, 2006, 03:33:21
Job time : 734 secs

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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 00:50:38 ; Search time 3759 Seconds  
(without alignments)  
248.934 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20

Sequence: 1 gcttgggtggcaacacat 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 1

Total number of hits satisfying chosen parameters: 82156240

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : EST:\*

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2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_hc:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_est7:\*

9: gb\_gss1:\*

10: gb\_gss2:\*

11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	100.0	238	AU023800	AU023800 AU023800
5	20	100.0	240	H82288	H82288 yv79h07.s1
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17	20	100.0	361	A1846721	A1846721 UI-M-AN1
18	20	100.0	382	AA035406	AA035406 xk26h09.s
19	20	100.0	388	AW274010	AW274010 xk26c05.x
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24	20	100.0	397	5	BP755053
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c	164	15	75.0	235	2	BB326112	BB326112	c 237	15	75.0	600	10	CL322869	CL322869
c	165	15	75.0	251	1	AV236517	AV236517	c 238	15	75.0	607	7	CV129240	CV129240
c	166	15	75.0	258	1	BB043559	BB043559	c 239	15	75.0	607	7	CV573233	CV573233
c	167	15	75.0	266	9	AO677203	HS_5514.A	c 240	15	75.0	608	7	CV130092	CV130092
c	168	15	75.0	269	1	AV325659	AV325659	c 241	15	75.0	610	3	BP758612	BP758612



C 242	15	75.0	610	7	CV572195	CV572195 od2a11.y	315	15	75.0	957	11	DQ040538
C 243	15	75.0	612	3	BP002831	BP002831	C 316	15	75.0	964	3	BQ229478
C 244	15	75.0	613	2	BE622702	BE622702	C 317	15	75.0	968	5	BQ229478
C 245	15	75.0	614	7	CR283230	CR283230	318	15	75.0	971	5	BQ682739
C 246	15	75.0	624	6	CB422065	CB422065 595134 MA	319	15	75.0	976	10	CL127403
C 247	15	75.0	639	9	BH834387	BH834387 BACPPE-L0	320	15	75.0	981	10	CL127470
C 248	15	75.0	643	5	BW270890	BW270890	321	15	75.0	987	1	AL569480
C 249	15	75.0	647	9	BH835070	BH835070 BACPPE7-B0	C 322	15	75.0	1002	10	CZ951230
C 250	15	75.0	648	10	AG966736	AG966736 Droophil	C 323	15	75.0	1023	3	BM460435
C 251	15	75.0	649	10	C2637518	C2637518 OM_Ba018	C 324	15	75.0	1027	8	DN575431
C 252	15	75.0	650	6	CB445030	CB445030 696270 MA	325	15	75.0	1029	6	CA478752
C 253	15	75.0	655	2	BF168549	BF168549 601775451	C 326	15	75.0	1069	2	BE963867
C 254	15	75.0	660	9	BZ750227	BZ750227 PUDBU3R7B	C 327	15	75.0	1095	10	AV404703
C 255	15	75.0	660	10	CW366570	CW366570 fbb001f0	C 328	15	75.0	1111	9	CC187166
C 256	15	75.0	664	3	BW179336	BW179336 UI-B-E00-	C 329	15	75.0	1114	8	DR144960
C 257	15	75.0	670	6	CB427738	CB427738 104_634_1	C 330	15	75.0	1171	2	BE420996
C 258	15	75.0	674	10	CZ771597	CZ771597 OC_Ba012	C 331	15	75.0	1217	8	DR144424
C 259	15	75.0	678	10	CN407574	CN407574 170006001	332	15	75.0	1218	8	DN804982
C 260	15	75.0	683	7	BU072133	BU072133 im54f08.y	333	15	75.0	1238	6	CD495465
C 261	15	75.0	690	5	BU072133	BU072133 im54f08.y	334	15	75.0	1313	3	BI562427
C 262	15	75.0	707	9	CC174377	CC174377 ZMBBEC029	C 335	15	75.0	1333	8	DN694526
C 263	15	75.0	709	6	CB444693	CB444693 695886 MA	C 336	15	75.0	1508	4	CR621279
C 264	15	75.0	712	6	CB422415	CB422415 595518 MA	C 337	15	75.0	1616	4	AK017910
C 265	15	75.0	720	10	CW622471	CW622471 OP_Ba002	C 338	15	75.0	2987	4	AK037533
C 266	15	75.0	721	7	CK223023	CK223023 70439877	339	15	75.0	4386	10	AV405198
C 267	15	75.0	726	5	BW433491	BW433491 BW433491	340	15	75.0	4386	10	AV405198
C 268	15	75.0	727	10	CW486655	CW486655 fbb001f2	C 341	14	70.0	109	10	AX891486
C 269	15	75.0	732	1	AJ819991	AJ819991 AJ819991	342	14	70.0	126	7	CK549660
C 270	15	75.0	733	1	AJ819991	AJ819991 AJ819991	343	14	70.0	148	2	BI278318
C 271	15	75.0	734	5	BU104194	BU104194 603006557	344	14	70.0	180	1	AV423825
C 272	15	75.0	737	8	CK6411381	CK6411381 UCRPT02_5	C 345	14	70.0	188	9	A2845817
C 273	15	75.0	742	10	CZ846572	CZ846572 OC_Ba023	C 346	14	70.0	196	1	AW401624
C 274	15	75.0	755	2	BG351150	BG351150 106804 MA	C 347	14	70.0	196	3	EM001994
C 275	15	75.0	761	7	CK364433	CK364433 AGENCOURT	C 348	14	70.0	208	9	CE214869
C 276	15	75.0	764	7	CV477581	CV477581 57485.1 D	349	14	70.0	209	9	AZ785736
C 277	15	75.0	766	10	CG350731	CG350731 OGLEF45TH	350	14	70.0	215	9	BH778624
C 278	15	75.0	776	1	B8023057	B8023057 BB023057	C 351	14	70.0	220	7	CF740719
C 279	15	75.0	777	10	CZ027462	CZ027462 OM_Ba000	C 352	14	70.0	242	1	AJ601563
C 280	15	75.0	778	8	DN514011	DN514011 1251033 M	353	14	70.0	242	7	CO873533
C 281	15	75.0	780	10	CW389454	CW389454 fbb001f0	354	14	70.0	267	2	BI276869
C 282	15	75.0	784	2	BG212399	BG212399 RST31986	C 355	14	70.0	277	1	AA833295
C 283	15	75.0	786	10	CZ763668	CZ763668 OC_Ba011	356	14	70.0	291	1	AV050281
C 284	15	75.0	790	9	BZ771311	BZ771311 mcb75a02.	C 357	14	70.0	297	2	BE500706
C 285	15	75.0	795	2	B1115894	B1115894 60286664	358	14	70.0	299	1	AI264523
C 286	15	75.0	795	2	BE3866290	BE3866290 601274543	359	14	70.0	307	1	AW183818
C 287	15	75.0	795	9	BH269934	BH269934 CH230-6M1	360	14	70.0	312	2	BE064238
C 288	15	75.0	799	7	CO488130	CO488130 GOQ205_B3	C 361	14	70.0	317	2	BE210876
C 289	15	75.0	800	7	CO488130	CO488130 BOvGen_16	C 362	14	70.0	319	6	CF034569
C 290	15	75.0	804	8	CK636290	CK636290 UCRPT02_1	C 363	14	70.0	319	10	CW736579
C 291	15	75.0	829	9	CO072519	CO072519 CSU-KG3r.	C 364	14	70.0	322	8	CK110573
C 292	15	75.0	835	6	CD247662	CD247662 AGENCOURT	365	14	70.0	330	1	AV815303
C 293	15	75.0	849	6	CF690239	CF690239 CCACZ64TO	C 366	14	70.0	332	3	BQ242966
C 294	15	75.0	851	10	CG821415	CG821415 SOYEU94TH	367	14	70.0	341	2	BF287647
C 295	15	75.0	853	10	CZ727604	CZ727604 OC_Ba005	C 368	14	70.0	355	5	BY009940
C 296	15	75.0	854	9	CCE23854	CCE23854 CH240_372	C 369	14	70.0	359	8	Z36258
C 297	15	75.0	859	6	CF716836	CF716836 CCAB844TF	C 370	14	70.0	360	5	BU571700
C 298	15	75.0	865	6	CB209520	CB209520 AGENCOURT	C 371	14	70.0	366	6	CA713251
C 299	15	75.0	871	10	CW781203	CW781203 OP_Ba008	372	14	70.0	368	3	BI429845
C 300	15	75.0	882	10	CZ884669	CZ884669 OC_Ba028	C 373	14	70.0	368	10	CE527985
C 301	15	75.0	883	6	CF066458	CF066458 Ac424_Amp	374	14	70.0	373	1	AW697493
C 302	15	75.0	884	8	DN583625	DN583625 90893580	C 375	14	70.0	373	7	CN210184
C 303	15	75.0	887	9	BZ240426	BZ240426 CH230-507	C 376	14	70.0	376	5	BY362535
C 304	15	75.0	891	2	BE974610	BE974610 601680615	C 377	14	70.0	376	5	CO5745
C 305	15	75.0	897	10	DU056016	DU056016 94353 Tom	C 378	14	70.0	377	1	AW415843
C 306	15	75.0	907	2	BF673821	BF673821 602135971	379	14	70.0	377	10	CZ2113192
C 307	15	75.0	907	10	CG771672	CG771672 TCB48_4_C	C 380	14	70.0	378	8	DN186872
C 308	15	75.0	913	5	BQ892605	BQ892605 AGENCOURT	C 381	14	70.0	382	1	AA835399
C 309	15	75.0	922	2	BF699925	BF699925 602127380	C 382	14	70.0	383	2	BE061335
C 310	15	75.0	923	9	BZ153865	BZ153865 CH230-300	C 383	14	70.0	389	2	BE488034
C 311	15	75.0	931	9	BZ771343	BZ771343 mcb76a02.	C 384	14	70.0	397	8	D24184
C 312	15	75.0	932	5	BU534072	BU534072 AGENCOURT	C 385	14	70.0	400	2	BE480612
C 313	15	75.0	941	2	BF784012	BF784012 602107856	C 386	14	70.0	402	2	BF899104
C 314	15	75.0	945	10	CL127356	CL127356 ISB1-92P2	C 387	14	70.0	402	3	BU243532

DQ040538	Pan trogl
BQ229478	AGENCOURT
BU527695	AGENCOURT
BQ682739	AGENCOURT
CL127403	ISB1-92H1
CL127470	ISB1-92I1
AL569480	AL569480
CZ951230	262076 To
BM460435	AGENCOURT
DN575431	91953185
CA478752	AGENCOURT
BE963867	601657635
AV404703	Homo sapi
CC187166	CH261-91M
DR144960	49075243
BE420996	HMM004_G0
DR144424	49135120
DN804982	76947221
CD495465	CD495465
BI562427	603255590
DN694526	CGX94-G01
CR621279	fulli-leng
AK017910	Mus muscu
AK037533	Mus muscu
AV405198	Homo sapi
AX405199	Pan trogl
AX891486	Arabidops
CK549660	swkx0_006
BI278318	UI-R-CW0-
AV423825	AV423825
AZ845817	2M0145113
AW401624	UI-HF-BK0
EM001994	103109991
CE214869	tigr-ges-
AZ785736	2M0029J20
BH778624	fzmb0013f0
CF740719	CR740719
AJ601563	AJ601563
CO873533	BovGen_01
BI276869	UI-R-CX0-
AA833295	ui05d07.r
AV050281	AV050281
BE500706	WHE0991-0
AI264523	q139h08.x
AW183818	xJ88c06.x
BE064238	CM4-BT030
BE210876	so54f12.y
CF034569	OCF6h05.Y
CW736579	MARC_8256
CK110573	E1050F09
AV815303	AV815303
BQ242966	Tae15020H
BF287647	EST452238
CA713251	wk3c.pk0
BI429845	fq75g07.x
CE527985	tigr-ges-
AW697493	ST61B12.P
CN210184	4116187.B
BY362535	BY362535
CO5745	CO5745 Huma
AW415843	50391.MAR
CZ2113192	AI1AA-aaaf4
DN186872	HO28B04w
AA835399	ak71911.B
BE061335	IL0-BT016
D24184	R1CR1494.R
BE480612	165748.BA
BF899104	CM2-MT018
BU243532	BU243532

388	14	70.0	402	9	AQ045047	AQ045047	RPCI11-34	C 461	14	70.0	533	10	CW333392	CW333392 104 831_1
389	14	70.0	403	9	A2439012	BP613246	de31f10.Y	462	14	70.0	534	7	CO070776	CO070776 GR_Ea27P
390	14	70.0	404	2	BF613246	AQ210223	HS_3229.A	463	14	70.0	535	7	CO077973	CO077973 GR_Ea40A
391	14	70.0	405	9	AQ210223	COL184873	EC28716.5	C 464	14	70.0	536	1	AU248157	AU248157 AU248157
392	14	70.0	409	7	CO184873	BZ874641	CH240_240	C 465	14	70.0	536	9	AZ882244	AZ882244 RPCI-23-1
393	14	70.0	409	9	BZ874641	CF046694	QKC28H12.	466	14	70.0	538	5	BW334329	BW334329 BW334329
394	14	70.0	410	6	CF046694	AQ0952216	Sheared.D	467	14	70.0	540	7	CN409294	CN409294 170006001
395	14	70.0	412	9	AQ0952216	AV768715	AV768715	C 468	14	70.0	545	1	AL809237	AL809237 AL809237
396	14	70.0	413	1	AV768715	AQ728310	HS_5446.B	C 469	14	70.0	545	2	BE517452	BE517452 WHE0626.B
397	14	70.0	417	9	AQ728310	BQ400403	604138929	C 470	14	70.0	545	9	AQ637851	AQ637851 922P1-18H
398	14	70.0	420	5	BQ400403	AQ462784	HS_5203.A	C 471	14	70.0	547	2	BG545941	BG545941 602573236
399	14	70.0	421	9	AQ462784	A1116062	uc14h08.r	472	14	70.0	547	7	CO998058	CO998058 pam01-17m
400	14	70.0	424	1	A1116062	AV415326	AV415326	473	14	70.0	548	2	BG040887	BG040887 NXSI_116
401	14	70.0	426	1	AV415326	AT665154	605007E04	474	14	70.0	548	7	CN409295	CN409295 170005321
402	14	70.0	427	1	AT665154	AV802341	AV802341	475	14	70.0	550	2	BE341206	BE341206 EST343507
403	14	70.0	427	1	AV802341	AV89928	vx70d09.r	C 476	14	70.0	550	6	CD866685	CD866685 AZ02.104C
404	14	70.0	430	1	AV89928	CD393170	Gm_CK1264	C 477	14	70.0	550	6	CF037882	CF037882 QCH13G05.
405	14	70.0	433	6	CD393170	BH785706	fzmb013f0	C 478	14	70.0	550	8	DT048239	DT048239 COT_CY_B0
406	14	70.0	434	9	BH785706	CN246034	EST011919	479	14	70.0	550	8	DT052233	DT052233 COT_EV_E0
407	14	70.0	437	7	CN246034	CN446278	CM390r.La	C 480	14	70.0	551	3	BP241503	BP241503 BP241503
408	14	70.0	437	7	CN446278	AV766417	AV766417	C 481	14	70.0	551	8	BU439513	BU439513 604143961
409	14	70.0	440	1	AV766417	BM895373	952073G11	C 482	14	70.0	553	8	DR708435	DR708435 Asn_09302
410	14	70.0	442	3	BM895373	R33983	15942.Lambd	C 483	14	70.0	554	6	CD887570	CD887570 G118.105K
411	14	70.0	443	8	R33983	CO100316	GR_Ea25K	484	14	70.0	556	3	BM092380	BM092380 sah12e05.
412	14	70.0	451	9	AQ667768	TS9594	vd99810_e1	485	14	70.0	556	8	DT107557	DT107557 JGI_ANNH8
413	14	70.0	453	7	CO100316	CD729501	4036623.1	486	14	70.0	556	9	AZ829391	AZ829391 2M0107101
414	14	70.0	455	8	TS9594	CV324723	CM4_FT010	C 487	14	70.0	557	9	AQ623755	AQ623755 HS_5319.A
415	14	70.0	456	6	CD729501	BM447165	DSA006G06	C 488	14	70.0	562	1	AW131487	AW131487 xf30d01.x
416	14	70.0	461	7	CV324723	CF848723	p8MA008xA	489	14	70.0	562	2	BG723175	BG723175 602690766
417	14	70.0	466	3	BM447165	AQ211502	HS_3243.A	490	14	70.0	563	5	BM165766	BM165766 BW615766
418	14	70.0	466	7	CF848723	B0117231	ESTf602807	491	14	70.0	565	3	BM895247	BM895247 952070H08
419	14	70.0	467	9	AQ211502	BU807219	haa13f04.	492	14	70.0	566	7	CO073255	CO073255 GR_Ea32M
420	14	70.0	469	3	B0117231	CL897843	ab946e06.	493	14	70.0	567	6	CD396029	CD396029 Gm_Ck1623
421	14	70.0	469	5	BU807219	BM967955	LM24HW008	494	14	70.0	568	1	AW615349	AW615349 AV615349
422	14	70.0	469	10	CL897843	BM967955	LM24HW008	C 495	14	70.0	572	1	AW973043	AW973043 EST385140
423	14	70.0	474	3	BM967955	CV610752	zcm28b04.	C 496	14	70.0	573	8	W15870	W15870 mb55a12.r1
424	14	70.0	474	6	CA704214	CV610752	zcm28b04.	C 497	14	70.0	574	1	AJ635934	AJ635934 AJ635934
425	14	70.0	478	3	BJ222411	BU886103	Na_L3_46D	C 498	14	70.0	574	6	CA626630	CA626630 w11n.pk01
426	14	70.0	478	7	BJ222411	CA704214	wk1c.pk0	C 499	14	70.0	575	3	BP006388	BP006388 BP006388
427	14	70.0	480	1	AJ469257	CA704214	wk1c.pk0	C 500	14	70.0	576	1	AA521736	AA521736 vi15f12.r
428	14	70.0	486	5	BU088613	CA704214	wk1c.pk0	C 501	14	70.0	581	5	BQ462228	BQ462228 HD01P167
429	14	70.0	488	7	CO086103	CA704214	wk1c.pk0	C 502	14	70.0	582	3	BP282426	BP282426 BP282426
430	14	70.0	490	3	BM345235	CA704214	wk1c.pk0	C 503	14	70.0	582	3	BP282458	BP282458 BP282458
431	14	70.0	493	1	AU124061	CA704214	wk1c.pk0	C 504	14	70.0	582	3	BP283061	BP283061 BP283061
432	14	70.0	494	5	BK672761	CA704214	wk1c.pk0	C 505	14	70.0	582	3	BP283149	BP283149 BP283149
433	14	70.0	495	3	BM324195	CA704214	wk1c.pk0	C 506	14	70.0	582	3	BP283678	BP283678 BP283678
434	14	70.0	499	10	CW097535	CA704214	wk1c.pk0	C 507	14	70.0	582	3	BP363148	BP363148 BP363148
435	14	70.0	500	1	AW074134	CA704214	wk1c.pk0	C 508	14	70.0	582	6	CD912426	CD912426 G550.114G
436	14	70.0	500	3	BP394524	CA704214	wk1c.pk0	C 509	14	70.0	583	3	BP351459	BP351459 BP351459
437	14	70.0	501	1	AW500065	CA704214	wk1c.pk0	C 510	14	70.0	585	2	BI285563	BI285563 UI-R-CW08
438	14	70.0	502	2	BG790687	CA704214	wk1c.pk0	C 511	14	70.0	585	5	C23111	C23111 C23111 Japa
439	14	70.0	502	5	BY380060	CA704214	wk1c.pk0	C 512	14	70.0	585	8	DN887408	DN887408 nag04907.
440	14	70.0	502	9	AQ519958	CA704214	wk1c.pk0	C 513	14	70.0	586	11	CR140186	CR140186 Reverse.s
441	14	70.0	504	10	CZ568763	CA704214	wk1c.pk0	C 514	14	70.0	587	3	BP364999	BP364999 BP364999
442	14	70.0	505	6	CB829921	CA704214	wk1c.pk0	C 515	14	70.0	588	3	BP350472	BP350472 BP350472
443	14	70.0	507	11	DE070674	CA704214	wk1c.pk0	C 516	14	70.0	588	6	CB636357	CB636357 OSUNEa01M
444	14	70.0	509	6	CA777302	CA704214	wk1c.pk0	C 517	14	70.0	588	7	CK010173	CK010173 2936558iC
445	14	70.0	510	2	BF624269	CA704214	wk1c.pk0	C 518	14	70.0	589	9	AZ840622	AZ840622 2M0138E14
446	14	70.0	511	1	AA017621	CA704214	wk1c.pk0	C 519	14	70.0	591	2	BG357233	BG357233 OV2_11.D1
447	14	70.0	512	3	BI751078	CA704214	wk1c.pk0	C 520	14	70.0	593	10	CW129985	CW129985 104_512_1
448	14	70.0	512	4	AK196189	CA704214	wk1c.pk0	C 521	14	70.0	594	3	BM062755	BM062755 KS01046H0
449	14	70.0	513	7	CN547433	CA704214	wk1c.pk0	C 522	14	70.0	594	6	CB348301	CB348301 CAB2SG000
450	14	70.0	517	6	CB188733	CA704214	wk1c.pk0	C 523	14	70.0	595	3	BJ612792	BJ612792 BJ612792
451	14	70.0	519	5	BK951008	CA704214	wk1c.pk0	C 524	14	70.0	595	9	AZ859980	AZ859980 2M0165114
452	14	70.0	519	7	CN203124	CA704214	wk1c.pk0	C 525	14	70.0	595	10	CE342219	CE342219 t1gr-g98s-
453	14	70.0	520	1	AV771243	CA704214	wk1c.pk0	C 526	14	70.0	596	3	BM100498	BM100498 EBna01.SQ
454	14	70.0	522	9	AQ539181	CA704214	wk1c.pk0	C 527	14	70.0	596	5	CA014595	CA014595 HT11M15r
455	14	70.0	522	9	AQ539181	CA704214	wk1c.pk0	C 528	14	70.0	597	5	BW331066	BW331066 BW331066
456	14	70.0	524	3	BP692640	CA704214	wk1c.pk0	C 529	14	70.0	597	10	CW736759	CW736759 MARC_8259
457	14	70.0	526	1	AW942989	CA704214	wk1c.pk0	C 530	14	70.0	598	11	PT018E03R	PT018E03R Parameticiu
458	14	70.0	526	9	AQ784262	CA704214	wk1c.pk0	C 531	14	70.0	600	2	BG487684	BG487684 FMI_73_A0
459	14	70.0	527	6	CA642568	CA704214	wk1c.pk0	C 532	14	70.0	600	2	BE365842	BE365842 P11_2.F11
460	14	70.0	532	1	AW720424	CA704214	wk1c.pk0	C 533	14	70.0	600	5	BW202619	BW202619 BW202619

534	14	70.0	600	7	CO070557	CO070557 GR_Ba27K	607	14	70.0	656	9	BH119617	BH119617 RPCI-24-2
535	14	70.0	600	10	AG924751	AG924751 Drosophil	608	14	70.0	656	9	CC36071	CC36071 ZMMBSb019
536	14	70.0	601	8	DN146324	DN146324 4844_A05	609	14	70.0	656	10	CW333393	CW333393 104_831_1
537	14	70.0	602	6	CA643625	CA643625 wreln.pk0	610	14	70.0	657	3	CD414634	CD414634 Gm_CK4683
538	14	70.0	605	6	CA067996	CA067996 SCQAD105	c 611	14	70.0	659	3	BJ269922	BJ269922 BJ269922
539	14	70.0	605	7	CV472874	CV472874 21027.1 D	c 612	14	70.0	660	6	CB517916	CB517916 aaalr5b5
540	14	70.0	605	9	AQ390942	AQ390942 CITBI-E1-	c 613	14	70.0	660	6	BZ120814	BZ120814 CH230-423
541	14	70.0	605	11	FR0031892	AL028261 Fugu rubr	c 614	14	70.0	660	10	CB553594	CB553594 tigr_g88-
542	14	70.0	606	6	CA067993	CA067993 SCQAD105	615	14	70.0	661	5	BW325447	BW325447 BW325447
543	14	70.0	607	3	BU555526	BU555526 BU555526	616	14	70.0	661	5	CB851363	CB851363 UI-CF-DU1
544	14	70.0	607	5	BU339151	BU339151 603515490	c 617	14	70.0	665	6	CD621505	CD621505 55049374H
545	14	70.0	608	6	CB348376	CB348376 CAB2SG000	c 618	14	70.0	666	5	BQ806619	BQ806619 WHE3581_B
546	14	70.0	608	10	CZ561754	CZ561754 1_p_bw014	619	14	70.0	667	3	BI751087	BI751087 Ta01_05Fo
547	14	70.0	609	8	CV880356	CV880356 MdEt6018K	c 620	14	70.0	670	6	CA088550	CA088550 SCRFAM212
548	14	70.0	610	1	AW447901	AW447901 BRY_1017	c 621	14	70.0	670	10	CZ034832	CZ034832 OM_Ba001
549	14	70.0	610	3	BM895264	BM895264 952073A11	622	14	70.0	671	8	DN991406	DN991406 TC118874
550	14	70.0	610	5	BQ605548	BQ605548 BRY_1017	623	14	70.0	674	7	CO105998	CO105998 GR_BD003
551	14	70.0	612	6	CA227125	CA227125 SCVPLP304	624	14	70.0	674	8	DT037845	DT037845 VVL132D10
552	14	70.0	616	2	BG717631	BG717631 602698252	c 625	14	70.0	674	9	BH925458	BH925458 odi33a08
553	14	70.0	616	5	BU984301	BU984301 HF03121r	626	14	70.0	674	9	BZ193790	BZ193790 CH230-331
554	14	70.0	617	3	BQ245698	BQ245698 TaE5201C	c 627	14	70.0	676	8	CX513722	CX513722 JGI_XZG58
555	14	70.0	618	6	CB843312	CB843312 M15B-3802	628	14	70.0	677	3	BI688660	BI688660 603311282
556	14	70.0	619	11	CR212154	CR212154 Reverse s	c 629	14	70.0	677	9	BZ537732	BZ537732 OCAJH77TF
557	14	70.0	620	11	CR344515	CR344515 mte1-78K1	c 630	14	70.0	677	10	CW137227	CW137227 104_523_1
558	14	70.0	621	10	CB722521	CB722521 tigr-g88-	c 631	14	70.0	678	7	CV055826	CV055826 BNEL1231h3
559	14	70.0	622	5	BU977459	BU977459 HAL1H12r	c 632	14	70.0	679	10	AG092171	AG092171 Pan trogl
560	14	70.0	622	5	BW324356	BW324356 BW324356	633	14	70.0	679	11	DE065979	DE065979 Oryzias 1
561	14	70.0	624	9	CS841915	CS841915 OGUY11TH	c 634	14	70.0	681	1	AV967402	AV967402 AV967402
562	14	70.0	624	5	BY721465	BY721465 BY721465	c 635	14	70.0	681	5	BQ766985	BQ766985 EBR008_SQ
563	14	70.0	624	6	CA165048	CA165048 SCBRZ312	c 636	14	70.0	681	6	CA839554	CA839554 MCT028G11
564	14	70.0	626	5	BU401442	BU401442 603485006	c 637	14	70.0	681	6	CF587815	CF587815 USDA-PP_1
565	14	70.0	626	10	CL938514	CL938514 OA_ABA005	c 638	14	70.0	682	6	CA289466	CA289466 SCAGFL800
566	14	70.0	628	6	CB861000	CB861000 RH03Jullw	c 639	14	70.0	682	7	CK062373	CK062373 59970r81c
567	14	70.0	628	10	BX145114	BX145114 Danilo rer	c 640	14	70.0	685	9	BH972740	BH972740 odj_46B01
568	14	70.0	629	2	BG721559	BG721559 602695167	c 641	14	70.0	686	5	BW372086	BW372086 BW372086
569	14	70.0	629	7	CV057382	CV057382 BNEL27b8	c 642	14	70.0	686	7	CV055855	CV055855 BNEL124c1
570	14	70.0	631	1	AA980353	AA980353 ua52b03_r	c 643	14	70.0	686	8	CX166023	CX166023 HESC2_35
571	14	70.0	632	1	AV405220	AV405220 AV405220	c 644	14	70.0	689	10	CG811493	CG811493 FSAAT54TR
572	14	70.0	632	3	BQ245502	BQ245502 TaE15023G	c 645	14	70.0	689	10	CZ064449	CZ064449 OM_Ba006
573	14	70.0	635	5	BW321657	BW321657 BW321657	c 646	14	70.0	690	2	BI210511	BI210511 EST528551
574	14	70.0	635	5	BW038196	BW038196 BW038196	c 647	14	70.0	690	9	CC579876	CC579876 CH240_374
575	14	70.0	636	6	CD403362	CD403362 Gm_CK2609	c 648	14	70.0	691	3	BQ247112	BQ247112 TaE15001C
576	14	70.0	636	10	CZ123223	CZ123223 OA_BA001	c 649	14	70.0	691	3	CF201623	CF201623 R880915N
577	14	70.0	637	5	BH199716	CB380988 tigr-g88-	c 650	14	70.0	691	8	CA899976	CA899976 JGI_CAA08
578	14	70.0	637	6	CA087970	BW199716 BW199716	c 651	14	70.0	691	8	DN227997	DN227997 MEST1213
579	14	70.0	637	7	CK547630	CA087970 SCQAM210	c 652	14	70.0	691	10	AG296053	AG296053 Mus muscu
580	14	70.0	639	1	AJ432029	CK547630 swk20_001	c 653	14	70.0	693	2	BE601684	BE601684 HVSMH009
581	14	70.0	640	1	AL857957	AJ432029 AJ432029	c 654	14	70.0	694	7	CN832627	CN832627 AGENCOURT
582	14	70.0	640	7	CV057374	AL857957 AL857957	c 655	14	70.0	694	9	BH924837	BH924837 odi56d12
583	14	70.0	641	5	CA009163	CV057374 BNEL27b10	c 656	14	70.0	695	5	BX484530	BX484530 DKFPz686G
584	14	70.0	641	6	CB888641	CA009163 HUI13F1Br	c 657	14	70.0	695	6	CA115556	CA115556 SCBLB103
585	14	70.0	642	6	CF005959	CB888641 G118.108L	c 658	14	70.0	696	6	CA198237	CA198237 SCRPAM110
586	14	70.0	643	3	BI602822	CF005959 QBI16f09	c 659	14	70.0	696	10	CG165902	CG165902 PUFZK07TB
587	14	70.0	643	6	CA215051	BI602822 603247182	c 660	14	70.0	697	10	CL180264	CL180264 104_390_1
588	14	70.0	643	8	DR087825	CA215051 SCRAD112	c 661	14	70.0	697	7	CN287516	CN287516 170005326
589	14	70.0	644	1	AV949479	DR087825 CAST100F1	c 662	14	70.0	698	5	BW294504	BW294504 BW294504
590	14	70.0	644	5	BX878778	AV949479 AV949479	c 663	14	70.0	699	1	AX895105	AX895105 AV895105
591	14	70.0	645	5	BX878778	BX978778 BX878778	c 664	14	70.0	699	7	CK066977	CK066977 72904r81c
592	14	70.0	645	10	CZ603783	BW25542 BW25542	c 665	14	70.0	700	7	CV054070	CV054070 BNEL106d4
593	14	70.0	646	6	CD403101	CD403101 Gm_CK2575	c 666	14	70.0	701	6	CF201680	CF201680 R880915N
594	14	70.0	647	5	BW251038	BW251038 BW251038	c 667	14	70.0	706	2	BE601912	BE601912 HVSMH010
595	14	70.0	648	5	BW330520	BW330520 BW330520	c 668	14	70.0	706	7	CO985202	CO985202 GM89503B1
596	14	70.0	650	5	BQ471619	BQ471619 BV02P12r	c 669	14	70.0	707	6	CD866766	CD866766 AZO2_104F
597	14	70.0	650	6	CA210410	CA210410 SCEPSB112	c 670	14	70.0	707	6	CF481796	CF481796 POLI_74_E
598	14	70.0	650	6	CA732290	CA732290 wlpic.pk0	c 671	14	70.0	707	8	DT085321	DT085321 JGI_ANNK3
599	14	70.0	650	10	CZ231128	CZ231128 AIAA-baf9	c 672	14	70.0	709	6	CA763250	CA763250 BR00008A
600	14	70.0	651	6	CV060466	CA388198 670351 NC	c 674	14	70.0	709	7	CV053850	CV053850 BNEL103h1
601	14	70.0	652	7	CV060466	CV060466 BNEL58d7	c 675	14	70.0	711	6	CF480441	CF480441 POLI_65_F
602	14	70.0	653	10	AG136288	AG136288 Pan trogl	c 676	14	70.0	711	7	CN011263	CN011263 WHE3882_A
603	14	70.0	654	5	BU991957	BU991957 HD08G17r	c 677	14	70.0	716	9	AZ908418	AZ908418 RPCI-24-2
604	14	70.0	655	5	BW234188	BW234188 BW234188	c 678	14	70.0	716	10	AG393890	AG393890 Mus muscu
605	14	70.0	655	5	BW234188		679	14	70.0	717	8	CX997039	CX997039 JGI_CAA06

680	14	70.0	717	9	CE038827	tigr-gss-	753	14	70.0	789	6	CB180222	AGENCOURT
c 681	14	70.0	718	8	CX910314	JGI_CAA2	c 754	14	70.0	790	8	CX899562	JGI_CAA8
c 682	14	70.0	719	11	CR053056	Forward	c 755	14	70.0	791	1	AJ612715	AJ612715
683	14	70.0	719	5	BW038201	BW038201	c 756	14	70.0	793	10	BX158897	BX158897
684	14	70.0	720	7	CV705629	UCRPT01_0	c 757	14	70.0	794	6	CD048804	CD048804
c 685	14	70.0	720	7	CV705629	UCRPT01_0	c 758	14	70.0	795	7	CK317001	CK317001
c 686	14	70.0	722	8	CX997040	JGI_CAAQ6	c 759	14	70.0	796	8	BZ788666	BZ788666
687	14	70.0	722	8	DT085786	JGI_ANNK2	760	14	70.0	796	8	DR857919	JGI_CARG3
c 688	14	70.0	725	8	CX484348	JGI_XZG34	761	14	70.0	796	9	BR2721016	PUDAU77TB
689	14	70.0	726	10	AG215665	AG215665	c 762	14	70.0	797	2	BG344447	HVSENG000
690	14	70.0	728	1	AA762751	AA762751	c 763	14	70.0	797	2	B1207408	EST525448
c 691	14	70.0	728	5	BX914879	BX914879	c 764	14	70.0	798	10	CEW21892	MARC_1131
692	14	70.0	728	5	BY710913	BY710913	c 765	14	70.0	798	8	CX910658	JGI_CAA2
693	14	70.0	728	8	DN507301	HL01020B2	c 766	14	70.0	800	9	CD779190	EST650551
694	14	70.0	729	3	B1560837	B1560837	767	14	70.0	800	6	CG660775	OGWFFS3TH
c 695	14	70.0	729	10	CW462017	CW462017	c 768	14	70.0	800	10	BX135746	BX135746
c 696	14	70.0	731	9	BZ687843	BZ687843	769	14	70.0	801	1	AW010317	ST04F05_P
697	14	70.0	731	10	CW517842	OP_Ba003	c 770	14	70.0	801	6	CB897606	tr1c011xn
c 698	14	70.0	732	5	BW331182	BW331182	771	14	70.0	801	7	CN498332	F08_02078
699	14	70.0	733	2	BE277305	BE277305	772	14	70.0	801	10	CZ286207	CG45f06_1
c 700	14	70.0	733	5	BW246179	BW246179	773	14	70.0	802	7	CN759569	ID0AAA25D
c 701	14	70.0	733	5	BW246179	BW246179	774	14	70.0	802	8	DT084924	JGI_A1ZU7
c 702	14	70.0	735	6	CA224869	CA224869	775	14	70.0	802	9	BZ755559	PURFS96TD
703	14	70.0	735	8	DR688913	DR688913	c 776	14	70.0	803	6	CB994865	AGENCOURT
c 704	14	70.0	736	5	BQ837963	BQ837963	c 777	14	70.0	804	8	CX325732	JGI_XZT14
c 705	14	70.0	737	8	DN041590	JGI_CAB1	c 778	14	70.0	804	8	CX921883	JGI_CAA8
706	14	70.0	739	9	B2537733	B2537733	c 779	14	70.0	806	6	CB631069	OS1TEb08G
c 707	14	70.0	740	7	CF867565	CF867565	780	14	70.0	808	6	CB994647	AGENCOURT
c 708	14	70.0	743	7	CR443180	CR443180	c 781	14	70.0	812	7	CN065247	C09_Ag2_P
c 709	14	70.0	743	10	CL797422	OR_CBA000	c 782	14	70.0	812	8	CX927674	JGI_CAA1
710	14	70.0	744	8	CX484349	CX484349	c 783	14	70.0	813	9	CG653748	OGFAL71TM
711	14	70.0	746	7	CR281948	CR281948	c 784	14	70.0	814	5	BU302972	603737815
712	14	70.0	748	8	DN587115	DN587115	c 785	14	70.0	816	8	CX914245	JGI_CAA4
713	14	70.0	749	6	CD485795	CD485795	c 786	14	70.0	816	9	CC016993	PUDGY68TD
714	14	70.0	751	8	DN015937	DN015937	c 787	14	70.0	818	10	CL755415	OR_BBa012
c 715	14	70.0	752	6	CA264701	CA264701	c 788	14	70.0	819	8	CV707667	gmrtDnR50
716	14	70.0	752	10	CL581907	CL581907	c 789	14	70.0	821	7	CV658757	Mdrt6015h
c 717	14	70.0	753	5	BX779141	BX779141	c 790	14	70.0	822	8	CX897486	JGI_CAA7
c 718	14	70.0	756	5	B0743229	B0743229	c 791	14	70.0	823	9	BZ864743	CH240_210
c 719	14	70.0	756	9	BZ276796	BZ276796	c 792	14	70.0	823	9	BZ978597	PURFZ81TB
c 720	14	70.0	758	5	BU366880	BU366880	c 793	14	70.0	824	10	CG195203	PURFJ12TB
721	14	70.0	759	2	BG702633	BG702633	c 794	14	70.0	825	9	BZ750229	PUDBU38TD
c 722	14	70.0	759	5	BX672760	BX672760	c 795	14	70.0	828	5	BX458229	BX458229
723	14	70.0	760	3	B1560595	B1560595	c 796	14	70.0	828	6	CA257816	SCCCT300
c 724	14	70.0	763	7	CK142371	CK142371	c 797	14	70.0	828	10	CZ280415	cp11c11_1
725	14	70.0	763	8	CX368412	CX368412	c 798	14	70.0	830	9	CC553258	CH240_459
c 726	14	70.0	764	6	CB655021	CB655021	c 799	14	70.0	830	10	CG132662	PUD1947TB
c 727	14	70.0	765	8	CX388999	CX388999	c 800	14	70.0	833	7	CK312184	SB02011A1
c 728	14	70.0	765	8	CX510994	CX510994	c 801	14	70.0	833	10	CZ240622	A1AA-aa2
c 729	14	70.0	767	10	CW440612	CW440612	c 802	14	70.0	835	8	CK806431	JGI_CAAJ1
730	14	70.0	769	7	CN093572	CN093572	c 803	14	70.0	835	9	BZ138565	CH230-288
731	14	70.0	770	2	BG297559	BG297559	c 804	14	70.0	836	2	BE277100	601178605
732	14	70.0	771	10	AG580785	AG580785	c 805	14	70.0	836	3	BP672312	BP_72312
c 733	14	70.0	772	8	CX928802	CX928802	c 806	14	70.0	840	7	CO115276	GR_Eb016
734	14	70.0	772	9	BZ748689	BZ748689	c 807	14	70.0	841	9	AZ530045	ENTCBB4TR
c 735	14	70.0	772	9	CC668904	CC668904	c 808	14	70.0	841	10	CW457855	fbdb001f2
c 736	14	70.0	773	10	CZ134021	CZ134021	c 809	14	70.0	844	8	DN975669	CT08_3_Ta
c 737	14	70.0	774	7	CJ342363	CJ342363	c 810	14	70.0	845	7	CO452007	MZCCL1017
738	14	70.0	774	8	DR036557	DR036557	c 811	14	70.0	845	8	CX381930	JGI_XZT53
c 739	14	70.0	775	9	CG934715	CG934715	c 812	14	70.0	847	10	CG214797	OG0GC31TH
740	14	70.0	775	10	CL550593	CL550593	c 813	14	70.0	848	8	DR426783	naw34906_1
c 741	14	70.0	776	10	CL653171	CL653171	c 814	14	70.0	849	9	CA060305	PULHKB8TF
742	14	70.0	777	3	BP707048	BP707048	c 815	14	70.0	849	9	CN093571	EC2BBABF
743	14	70.0	778	1	AJ568530	AJ568530	c 816	14	70.0	851	7	CN093571	EC2BBABF
c 744	14	70.0	778	10	CG682797	CG682797	c 817	14	70.0	852	3	B1562686	603256733
c 745	14	70.0	780	5	BQ802996	BQ802996	c 818	14	70.0	852	6	CB995723	AGENCOURT
c 746	14	70.0	780	5	BZ286048	BZ286048	c 819	14	70.0	852	7	CO936392	AGENCOURT
c 747	14	70.0	786	8	CX921078	CX921078	c 820	14	70.0	853	9	CX381929	JGI_XZT53
c 748	14	70.0	786	9	CC395505	CC395505	c 821	14	70.0	854	10	CG313974	OG3ACB9TH
749	14	70.0	787	7	CV145775	CV145775	c 822	14	70.0	854	10	CG026250	PGNAE78TR
c 750	14	70.0	787	8	CX806430	CX806430	c 823	14	70.0	859	8	CX928352	JGI_CAA1
c 751	14	70.0	788	5	BQ788942	BQ788942	c 824	14	70.0	861	8	CV766210	FGA506059
c 752	14	70.0	788	10	BX157287	BX157287	c 825	14	70.0	862	5	BU296550	603742202

C 826	14	70.0	862	8	CX917392	JGI_CAAAG6	C 899	14	70.0	961	10	CL999101	CL999101 ZMMBH6001
C 827	14	70.0	862	10	CW716930	A1A-aab7	C 900	14	70.0	962	10	CG135889	CG135889 PUTU45TB
C 828	14	70.0	867	8	DN081756	JGI_CABDI	C 901	14	70.0	964	5	BU411645	BU411645 603153436
C 829	14	70.0	867	9	AZ535579	ENTCF35TF	C 902	14	70.0	966	2	BG762974	BG762974 602735029
C 830	14	70.0	867	10	CL503423	SAIL_724	C 903	14	70.0	966	5	BQ713154	BQ713154 AGENCOURT
C 831	14	70.0	868	2	BF541457	602069289	C 904	14	70.0	980	9	C443038	C443038 PUHHC65TB
C 832	14	70.0	869	5	BX750383	BX750383	C 905	14	70.0	987	3	BM050726	BM050726 603633507
C 833	14	70.0	869	8	CV768349	FGAS06274	C 906	14	70.0	987	5	BU512432	BU512432 AGENCOURT
C 834	14	70.0	869	9	BZ810231	PUFFC54TB	C 907	14	70.0	988	2	BB876299	BB876299 601486616
C 835	14	70.0	870	8	CX915585	JGI_CAAAN5	C 908	14	70.0	989	5	BU177551	BU177551 AGENCOURT
C 836	14	70.0	872	10	CG225588	OGTGH87TV	C 909	14	70.0	992	5	BQ708400	BQ708400 AGENCOURT
C 837	14	70.0	873	10	CZ928653	ENTG94TF	C 910	14	70.0	992	10	CG165903	CG165903 PUP2X07TD
C 838	14	70.0	874	10	CG683120	OSJNEF11N	C 911	14	70.0	995	5	BQ888754	BQ888754 AGENCOURT
C 839	14	70.0	874	6	CB683462	WS0266.B2	C 912	14	70.0	1000	6	CD558636	CD558636 AGENCOURT
C 840	14	70.0	874	8	DR566134	AG876930	C 913	14	70.0	1003	9	CC253957	CC253957 CH261-79B
C 841	14	70.0	874	10	AG876930	Oryza sat	C 914	14	70.0	1007	2	BF133515	BF133515 601646052
C 842	14	70.0	875	9	BZ978599	PUGF281TD	C 915	14	70.0	1007	5	BQ712246	BQ712246 AGENCOURT
C 843	14	70.0	876	2	BG394249	602456448	C 916	14	70.0	1016	8	DN940319	DN940319 8678.3 AF
C 844	14	70.0	876	9	BZ044879	lkf54f11	C 917	14	70.0	1017	9	CG685070	CG685070 OGULH65TV
C 845	14	70.0	877	5	BU374958	603590611	C 918	14	70.0	1018	5	BY703573	BY703573 BY703573
C 846	14	70.0	881	5	BU382210	603855968	C 919	14	70.0	1019	3	BQ049166	BQ049166 AGENCOURT
C 847	14	70.0	883	6	CA814916	CA12E1201	C 920	14	70.0	1023	7	CN645462	CN645462 ILLUMIGEN
C 848	14	70.0	883	9	CZ516548	CH240_362	C 921	14	70.0	1024	5	BQ710263	BQ710263 AGENCOURT
C 849	14	70.0	883	10	CZ536806	CZ536806 SRAA-aad0	C 922	14	70.0	1027	10	CG881937	CG881937 ZMMBB049
C 850	14	70.0	884	6	CD573953	UCRPT01_0	C 923	14	70.0	1030	10	CL116459	CL116459 ISB1-6511
C 851	14	70.0	884	7	CR981226	CR981226	C 924	14	70.0	1061	5	BU200992	BU200992 603104179
C 852	14	70.0	884	8	DR036558	47097.3 L	C 925	14	70.0	1066	2	BG832182	BG832182 602765347
C 853	14	70.0	885	9	CZ516720	CH240_362	C 926	14	70.0	1078	10	CL039353	CL039353 CH216-47M
C 854	14	70.0	885	10	AG877164	Oryza sat	C 927	14	70.0	1080	11	DQ040537	DQ040537 Homo sapi
C 855	14	70.0	890	5	BX327839	BX327839	C 928	14	70.0	1085	3	BM909092	BM909092 AGENCOURT
C 856	14	70.0	890	6	CZ353089	SCJLFLA09	C 929	14	70.0	1092	6	CB592554	CB592554 AGENCOURT
C 857	14	70.0	892	6	CD779189	EST650550	C 930	14	70.0	1092	9	CC302910	CC302910 CH261-52H
C 858	14	70.0	892	8	W30144	mc27h09.r1	C 931	14	70.0	1094	5	BQ887568	BQ887568 AGENCOURT
C 859	14	70.0	892	9	CA443041	PUHRC65TD	C 932	14	70.0	1110	6	CF242541	CF242541 AGENCOURT
C 860	14	70.0	893	6	CD245976	CD245976 AGENCOURT	C 933	14	70.0	1112	10	CZ364475	CZ364475 ZMMBP0143
C 861	14	70.0	893	7	CK870361	AGENCOURT	C 934	14	70.0	1116	2	BS906138	BS906138 601497186
C 862	14	70.0	893	9	CG653742	CG653742 OGTAL71TC	C 935	14	70.0	1127	9	CL193298	CL193298 CH261-180
C 863	14	70.0	895	5	BX778015	BX778015	C 936	14	70.0	1128	10	CW930402	CW930402 EDC233TF
C 864	14	70.0	895	10	AG159093	AG159093 Pan trogl	C 937	14	70.0	1129	8	DR143641	DR143641 49108859
C 865	14	70.0	896	7	CQ930270	AGENCOURT	C 938	14	70.0	1149	8	DR147106	DR147106 49272374
C 866	14	70.0	896	9	CG694719	OGLBQ81TV	C 939	14	70.0	1177	9	CC228614	CC228614 CH261-45J
C 867	14	70.0	898	10	AG873796	Oryza sat	C 940	14	70.0	1201	7	CK209706	CK209706 FGAS02148
C 868	14	70.0	900	7	CA453107	CO453107 MZCCL1018	C 941	14	70.0	1206	10	AG163926	AG163926 Pan trogl
C 869	14	70.0	900	8	DN081755	DN081755 JGI_CABDI	C 942	14	70.0	1207	5	BU462668	BU462668 60368138
C 870	14	70.0	901	2	BG760411	BG760411 602716834	C 943	14	70.0	1227	7	CK211045	CK211045 FGAS02287
C 871	14	70.0	901	5	BX327047	BX327047	C 944	14	70.0	1257	5	BU330224	BU330224 603494154
C 872	14	70.0	901	6	CD246686	CD246686 AGENCOURT	C 945	14	70.0	1275	10	CL965865	CL965865 OatFCC012
C 873	14	70.0	911	9	BZ668924	PUBCX89TD	C 946	14	70.0	1280	10	AG435596	AG435596 Mus muscu
C 874	14	70.0	911	10	CG236341	CG236341 OG3DO69TH	C 947	14	70.0	1317	8	DN694146	DN694146 CGX22-EL0
C 875	14	70.0	911	11	CR230253	CR230253 Forward B	C 948	14	70.0	1344	10	CL650080	CL650080 CH213-275
C 876	14	70.0	914	5	BX764118	BX764118	C 949	14	70.0	1359	6	CB308945	CB308945 AGENCOURT
C 877	14	70.0	916	6	CF226157	CF226157 AGENCOURT	C 950	14	70.0	1368	8	CX106125	CX106125 B1125C03
C 878	14	70.0	917	10	CZ512488	CZ512488 GMW2-37L1	C 951	14	70.0	1527	4	AK009500	AK009500 Mus muscu
C 879	14	70.0	918	10	CG920204	CG920204 MBEK10TF	C 952	14	70.0	1565	2	BE421561	BE421561 HWM0115B
C 880	14	70.0	919	6	CF216534	AGENCOURT	C 953	14	70.0	1692	2	BF234458	BF234458 602028253
C 881	14	70.0	921	5	BU318035	BU318035 603851650	C 954	14	70.0	2022	10	AY417450	AY417450 Homo sapi
C 882	14	70.0	924	9	CG637048	OGUKV12TV	C 955	14	70.0	2048	7	CN970564	CN970564 18061.123
C 883	14	70.0	924	9	CC995831	ZUACG87TH	C 956	14	70.0	2705	11	DQ030436	DQ030436 Homo sapi
C 884	14	70.0	925	10	CG448340	OG5EJ06TV	C 957	14	70.0	3728	4	AK036402	AK036402 Mus muscu
C 885	14	70.0	928	7	CK125211	BE8182410	C 958	14	70.0	3728	4	AK036784	AK036784 Mus muscu
C 886	14	70.0	928	10	CG313989	CG313989 OG3AC89TV	C 959	14	70.0	5194	4	CR859162	CR859162 Pongo pyg
C 887	14	70.0	934	6	CF407156	CF407156 CH3#046 F	C 960	14	70.0	5693	4	CR627061	CR627061 Homo sapi
C 888	14	70.0	934	7	CN063601	Ag2_P43 A	C 961	13	65.0	92	9	BH630861	BH630861 1007095C0
C 889	14	70.0	936	10	CZ998510	187882 To	C 962	13	65.0	93	6	CF358169	CF358169 rm87c09.Y
C 890	14	70.0	939	10	CL076393	CH216-139	C 963	13	65.0	105	9	AZ519973	AZ519973 RPI-11-7
C 891	14	70.0	940	10	CZ334544	CZ334544 ZMMBP0043	C 964	13	65.0	105	9	CC407041	CC407041 PUHQZ93TB
C 892	14	70.0	945	10	CG308521	CG308521 OGZAM31TH	C 965	13	65.0	109	9	BH143820	BH143820 TDGE287TH
C 893	14	70.0	946	6	CD386447	AGENCOURT	C 966	13	65.0	110	1	AI349564	AI349564 qp73c09.x
C 894	14	70.0	949	9	CG685063	OGULH65TH	C 967	13	65.0	110	2	BF942085	BF942085 nae86e08
C 895	14	70.0	952	5	BX411337	BX411337	C 968	13	65.0	133	3	BJ749105	BJ749105 BJT49105
C 896	14	70.0	954	10	CZ693499	L008 SP23	C 969	13	65.0	140	7	CO855515	CO855515 LM SL5_00
C 897	14	70.0	955	10	CG316879	OGVBR50TV	C 970	13	65.0	141	9	AZ758345	AZ758345 1M050L13
C 898	14	70.0	958	6	CA275372	SCBPSD103	C 971	13	65.0	148	2	BF367767	BF367767 RC2-GN003

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972 13 55.0 148 6 CF308169 ABP--01-O
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976 13 55.0 157 8 DN985850 MSU 28F.2
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978 13 55.0 161 1 AA887300 oJ48908.s
979 13 55.0 161 10 CW346948 fdbb001f0
c 980 13 55.0 163 10 BX998489 Forward s
981 13 55.0 165 9 AZ315631 1M0032K24
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985 13 55.0 175 5 BW475846 BW475846
c 986 13 55.0 175 3 BN874193 laa02F08.
c 987 13 55.0 177 1 AV552054 AV552054
c 988 13 55.0 182 7 CN795023 DMP0153 M
989 13 55.0 182 10 AG213005 Oryza sat
c 990 13 55.0 191 2 BF460685 UI-M-CG0p
991 13 55.0 194 1 AU304561 AU304561
c 992 13 55.0 199 1 BB183251 BB183251
c 993 13 55.0 200 10 CL274920 CL274920 Ggal.88b
994 13 55.0 204 2 BE955497 UI-M-BH4-
c 995 13 55.0 204 10 AG205720 Oryza sat
996 13 55.0 205 8 DN251640 ACAB-aab9
c 997 13 55.0 206 5 BY154361 BY154361
c 998 13 55.0 207 5 BQ610872 sap51h05.
c 999 13 55.0 208 10 AG955822 Drosophil
c1000 13 55.0 209 9 A2587012 1M0394B21

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## ALIGNMENTS

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RESULT 1
W35284 191 bp mRNA linear EST 13-MAY-1996
LOCUS W35284.1 GI:1317280
DEFINITION W35284.1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
(HUMAN); mRNA sequence.
ACCESSION W35284.1
VERSION W35284.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 191)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfig,T., Soares,M., Tan,F.,
Trevasakis,B., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
JOURNAL The WashU-Merck EST Project
COMMENT Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: mob.REG+ET
High quality sequence stop: 1.
FEATURES
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1. .191
/organism="Homo sapiens"
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/clone="IMAGE:321607"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares parathyroid tumor NbHPA"
/notes="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer
[5'-TGTTCAATCTGAGTGGGCGCGCACCAATTTTTTTTTTTTTTTT
TTTTT-3'], double-stranded cDNA was size selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."
ORIGIN
Query Match 100.0%; Score 20; DB 8; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTTTGGTTGGGCAACACAT 20
|||||
Db 158 GCTTTGGTTGGGCAACACAT 177
RESULT 2
AW496823 230 bp mRNA linear EST 01-MAR-2000
LOCUS AW496823
DEFINITION d1 Neuronal Differentiation of the NT2/D1 cell line. Homo sapiens
cDNA 3' similar to forkhead protein (FKHR), mRNA sequence.
ACCESSION AW496823
VERSION AW496823.1 GI:7118853
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 230)
AUTHORS Bevolt,M.
JOURNAL Analysis of gene expression during neuronal differentiation of
NT2/D1 cells
COMMENT Unpublished (2000)
Contact: Bevolt M
Department of Growth and Reproduction GR-5064
Copenhagen University Hospital
Blegdamsvej 9, 2100 Copenhagen, Denmark
Tel: +45 35455081
Fax: +45 35456054
Email: maja@biobase.dk
The EST is up regulated followed by a down regulation, during
neuronal differentiation of the NT2/D1 cell line.
PCR Primers
FORWARD: AAGCTTCGACTGT
BACKWARD: AAGCTTTTITTTT
Seq primer: T7, CV5-TAATACGACTCACTATAGGGCC
High quality sequence stop: 230.
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/cell_line="NT2/D1"
/clone_lib="Neuronal Differentiation of the NT2/D1 cell
line."
/notes="The EST is derived from direct sequencing of a
Differential Display fragment. Laboratory manuals are
available from http://www.biobase.dk/-ddbbase"

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## ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 0.3;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTGGCAACACAT 20  
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 Db 139 GCTTTGGTGGCAACACAT 158

## RESULT 3

T85080 231 bp mRNA linear EST 17-MAR-1995  
 LOCUS ye03g09.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
 DEFINITION IMAGE:116704 3' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3  
 (HUMAN); mRNA sequence.

## ACCESSION

VERSION T85080.1 GI:713432

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

## REFERENCE

1 (bases 1 to 231)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 Insert Size: 914

High quality sequence stops: 33 Source: IMAGE Consortium, LLNL This  
 clone is available royalty-free through LLNL; contact the IMAGE  
 Consortium (info@image.llnl.gov) for further information.

Insert Length: 914 Std Error: 0.00

Seq primer: -21ml3

High quality sequence stop: 33.

## FEATURES

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 /db\_xref="taxon:9606"  
 /clone="IMAGE:116704"  
 /sex="male"  
 /dev\_stage="20 week-post conception fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares fetal liver spleen INFLS"  
 /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)  
 with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;  
 1st strand cDNA was primed with a Pac I - oligo(dT) primer  
 [5'-AAGTGGAGATTAATTAAGATCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Pac I and cloned into the Pac I  
 and Eco RI sites of the modified pT7T3 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaldo."

## ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 0.3;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTGGCAACACAT 20

Db 167 GCTTTGGTGGCAACACAT 186  
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## RESULT 4

AU023800 238 bp mRNA linear EST 20-OCT-1998  
 LOCUS AU023800 Mouse unfertilized egg cDNA Mus musculus cDNA clone  
 DEFINITION J0439B03 3', mRNA sequence.

## ACCESSION

VERSION AU023800.1 GI:3394147

## KEYWORDS

EST.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 238)

## AUTHORS

Ko, M.S.H., Kitchen, J.R., Wang, X., Threat, T.A., Sun, T., DePalma, G.E.,  
 Liang, Y., Kargul, G.J., Sharara, R. and Doi, H.

## TITLE

Systematic analyses of genes expressed in unfertilized mouse eggs  
 (The ERATO/Doi Project at Wayne State University) (Ko, M.S.H. et  
 al.)

## JOURNAL

Unpublished (1998)

## COMMENT

Contact: Hirofumi Doi

Doi Biosymmetry Project, ERATO

Japan Science and Technology Corporation (JST)

WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan

Email: hdoibioa.jst.go.jp.

## FEATURES

source

1..238  
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## ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.3;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTGGCAACACAT 20

|||||

Db 156 GCTTTGGTGGCAACACAT 175

## RESULT 5

H82288 240 bp mRNA linear EST 09-NOV-1995  
 LOCUS YV79h07.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone  
 DEFINITION IMAGE:248989 3' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3  
 (HUMAN); mRNA sequence.

## ACCESSION

VERSION H82288.1 GI:1060377

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

## REFERENCE

1 (bases 1 to 240)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK

Washington University School of Medicine



4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 1

High quality sequence starts: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Seq primer: Promega -21m13

High quality sequence stop: 1.

Location/Qualifiers

1. .240

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3866695"

/db\_xref="taxon:9606"

/clone="IMAGE:24989"

/sex="Male"

/tissue\_type="melanocyte"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares melanocyte 2NBRM"

/note="Vector: pRT3D (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGGAGCGCGCAGTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pRT3 vector

(Pharmacia). Library constructed by Bento Soares and

M.Patima Bonaldo. RNA from normal foreskin melanocytes

(FS374) was kindly provided by Dr. Anthony P. Albino."

#### FEATURES

source

FEATURES  
source

1. .255

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="9530049D21"

/sex="male"

/tissue\_type="urinary bladder"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="RIKEN full-length enriched, adult male urinary

bladder"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was

prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in

RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5'

GAGAGAGAAGCATCCAGAGCTTTTTTTTTTTT 3'], cDNA was

prepared by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full-length by

cap-trapper. cDNA went through one round of normalization

to Rot = 20.0 and subtraction to Rot = 370.0. Second

strand cDNA was prepared with the primer adapter of

sequence [5' GAGAGAGATTCGAGTTAATAATATCCCGCCCCCCC

3'] cDNA was cleaved with XhoI and BamHI. Vector: a

modified pBluescript KS(+) after bulk excision from

Lambda FLC 1."

#### ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 255;

Best Local Similarity 100.0%; Pred. No. 0.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGGTGGGCAACACAT 20

|||||

Db 100 GCTTGGTGGGCAACACAT 81

#### RESULT 7

AV318369/c

LOCUS

DEFINITION

AV318369

musculus cDNA clone 5930401120 3' similar to AF114258 Mus musculus

forkhead protein FKHR1 (FKHR1) mRNA, mRNA sequence.

AV318369

ACCESSION

VERSION

KEYWORDS

EST.

TITLE

RIKEN Mouse ESTs (Konno,H., et al.)

#### JOURNAL

COMMENT

Unpublished (2000)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoaka,S.,

Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermotabilization and thermoactivation of thermolabile enzymes by

trehalose and its application for the synthesis of full length

cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,

Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,

Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)

Please visit our web site (http://genome.rtc.riken.go.jp) for

further details.

Location/Qualifiers

**SOURCE**  
ORGANISM  
**REFERENCE**  
AUTHORS

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 269)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,  
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,  
Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,  
Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,  
Matsumura,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,  
Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,  
Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,  
Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N.,  
Tsunoda,Y., Watabiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,  
Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Konno,H., et al. 1999)  
Unpublished (1999)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gs.c.riken.jp, URL:http://genome.gsc.riken.jp/  
Sasaki,N., Izawa,M., Watabiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,  
Mateuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and  
Hayashizaki,Y.

**TITLE**  
JOURNAL  
COMMENT

Transcriptional sequencing: A method for DNA sequencing using RNA  
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
Itoh,M., Kiteunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,  
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,  
Okazaki,Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

**FEATURES**  
source

Location/Qualifiers  
1..269  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="CS7BL/6J"  
/db\_xref="taxon:10090"  
/clone="5930401120"  
/sex="mixed"  
/tissue\_type="forelimb"  
/dev\_stage="13 days embryo"  
/lab\_host="DH10B"  
/clone\_lib="RIKEN full-length enriched, 13 days embryo  
forelimb"  
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAAGCATCCACAGCTCTTTTATTTTTTNNV 3']. cDNA was  
prepared by using thermostable thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 10.0 and subtraction to Rot = 100.0. Second  
strand cDNA was prepared with the primer adapter of  
sequence [5' GAGAGAGATTCTCGATTAAATAATTAATCCCCCCCCCCC  
3'] cDNA was cloned into the XhoI and BamHI sites.  
Vector: a modified pBluescript KS(+) after bulk excision  
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:  
BamHI."

**QUERY MATCH**  
Best Local Similarity 100.0%; Score 20; DB 1; Length 269;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY**  
1 GCTTGTTGGTGGCAACACAT 20  
|||||  
121 GCTTGTTGGTGGCAACACAT 102

**RESULT 8**  
AV338311/c  
LOCUS  
DEFINITION  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
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KEYWORDS  
ORGANISM  
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JOURNAL  
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KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
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forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
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JOURNAL  
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AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
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JOURNAL  
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AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
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ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
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forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
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VERSION  
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AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
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forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
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KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
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AV338311  
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AUTHORS  
TITLE  
JOURNAL  
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musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
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KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430408119 3' similar to AF114258 Mus musculus  
forward protein FKHR1 (FKHR1) mRNA, mRNA sequence.  
AV338311  
VERSION  
EST.  
SOURCE  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AV338311 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 643040811

## ORIGIN

/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAATTAATCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda F1C I. Cloning sites, 5' end: Sali; 3' end: BamHI."

## ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 287;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGGTGGCAACACAT 20  
|||||  
Db 132 GCTTGGTGGCAACACAT 113

## RESULT 9

CF135310  
LOCUS  
DEFINITION UI-HP-BR0p-ary-a-08-0-UI.1 NIH\_MGC\_52 Homo sapiens cDNA clone IMAGE:30554023 5', mRNA sequence.

ACCESSION CF135310  
VERSION CF135310.1 GI:33250754  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 314)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL PUBMED 889548  
COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565

Email: bento-soares@uiowa.edu  
Tissue Procurement: Louis Staudt  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/humanfl.html>  
Seq primer: pYX-5.

## FEATURES

## source

Location/Qualifiers  
1..314  
/organism="Homo sapiens"  
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/clone="IMAGE:30554023"  
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/cell\_type="germinal center B cells"  
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/lab\_host="DH10B (LTI)"  
/clone\_lib="NIH\_MGC\_52"

/note="Vector: p77T3-Pac; Site 1: NotI; Site 2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(7.4-9.5kb). Directionally cloned. Cells provided by  
Louis M. Staudt, Ph.D. Library preparation by Maria de  
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 314;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCTTGGTGGCAACACAT 20  
|||||  
Db 168 GCTTGGTGGCAACACAT 187

## RESULT 10

## BU783931/c

## LOCUS

DEFINITION BU783931  
in11901.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:6124224  
3' similar to SW:FKHR\_HUMAN Q12778 FORK HEAD DOMAIN PROTEIN FKHR.

[1] : mRNA sequence.

ACCESSION BU783931

VERSION BU783931.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## AUTHORS

1 (bases 1 to 316)  
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Page,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,S., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T., Jackson,Y. and Bowers,Y.  
Endocrine Pancreas Consortium

## TITLE

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. J. Ferrer In vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)  
Possible reversed clone: similarity on wrong strand

Seq primer: -40UP from Gibco.

Location/Qualifiers

## FEATURES

## source

1..316  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:6124224"  
/tissue\_type="insulinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="Human insulinoma"  
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1: XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington University protocol  
([http://genome.wustl.edu/est/lambda\\_protocol.shtml](http://genome.wustl.edu/est/lambda_protocol.shtml)).  
Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: This is a Washington University Pancreas EST project library. "



SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 349)  
Henrich, J., Hermanns, J., Kranz, H., Loebbert, R., Schlueter, T.,  
Schuette, D., Weindel, M., Heil, O., Ebert, L., Neubert, P., Peters, M.,  
Radelof, U., Schneider, D. and Korn, B.  
Mouse ArrayTAG cDNA (LION)  
Unpublished (2003)  
Contact: Ina Kolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; LIONp462B0882.  
RZPDLIB;  
Mouse ArrayTAG cDNA (LION)  
http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi?response?libNo=4  
62 Contact: Ina Kolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
RP: CAGGAACAGCTATGAC.  
FEATURES  
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Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="LIONp462B0882"  
/lab\_host="DH10B"  
/clone\_lib="pbluescript Lion"  
ORIGIN  
Query Match 100.0%; Score 20; DB 5; Length 349;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCTTTGGTTGGGCAACACAT 20  
|||||  
Db 161 GCTTTGGTTGGGCAACACAT 180  
RESULT 14  
W32908/c  
LOCUS  
DEFINITION  
zc07d04.t1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone  
IMAGE:321607 5' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3  
(HUMAN); mRNA sequence.  
ACCESSION  
W32908  
VERSION  
W32908.1 GI:1314963  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 353)  
Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P.,  
Trevaaskis, B., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu  
This clone is available royalty-free through LILN; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: mob.REGA+ET  
High quality sequence stop: 328.  
FEATURES  
source  
Location/Qualifiers  
1..353  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="CDB:1259265"  
/db\_xref="taxon:9606"  
/clone="IMAGS:321607"  
/tissue\_type="parathyroid tumor"  
/dev\_stage="adult"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares parathyroid tumor NbHPA"  
/notes="Organ: parathyroid gland; Vector: pRTT3D  
(Pharmacia) with a modified polylinker; Site 1: Not I;  
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -  
oligo(dT) primer  
[5'-TGTTACCAATCTGAAGTGGGCGCGCCACCAATTTTTTTTTTTTTTTT  
TTTTT-3'] double-stranded cDNA was size selected, ligated  
to Eco RI adapters (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of a modified pRTT3  
vector (Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid  
adenomas was kindly provided by Dr. Stephen Marx, National  
Institute of Diabetes and Digestive and Kidney Diseases,  
NIH."  
ORIGIN  
Query Match 100.0%; Score 20; DB 8; Length 353;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCTTTGGTTGGGCAACACAT 20  
|||||  
Db 180 GCTTTGGTTGGGCAACACAT 161  
RESULT 15  
CR469238  
LOCUS  
DEFINITION  
CR469238 Rat pBluescript Lion Rattus norvegicus cDNA clone  
LIONp463E08441 3', mRNA sequence.  
ACCESSION  
CR469238  
VERSION  
CR469238.1 GI:49601587  
KEYWORDS  
EST.  
SOURCE  
Rattus norvegicus (Norway rat)  
ORGANISM  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Rattus.  
1 (bases 1 to 355)  
Henrich, J., Hermanns, J., Kranz, H., Loebbert, R., Schlueter, T.,  
Schuette, D., Weindel, M., Heil, O., Ebert, L., Neubert, P., Peters, M.,  
Radelof, U., Schneider, D. and Korn, B.  
Rat ArrayTAG cDNA  
Unpublished (2004)  
Contact: Inge Arlart  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Email: www.rzpd.de  
RZPD; LIONp463E08441.  
RZPDLIB;  
Rat ArrayTAG cDNA  
http://www.rzpd.de/cgi-  
bin/products/showLib.pl.cgi?response?libNo=463 Contact: Inge Arlart  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 100  
Fax: +49 30 32639 111

www.rzpd.de  
This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
RP: CAGGAACAGCTATGAC.

## FEATURES

source Location/Qualifiers

1..355  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="BfOMP463E08441"  
/lab\_host="DH10B"  
/clone\_lib="Rat pBluescript Lion"

## ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 355;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGGTGGGCAACACAT 20

|||||

Db 159 GCTTGGTGGGCAACACAT 178

## RESULT 16

H99327

LOCUS

DEFINITION

Yx23c01.s1 Soares melanocyte 2NBM Homo sapiens cDNA clone  
IMAGE:262560 3' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3  
(HUMAN); mRNA sequence.

ACCESSION

H99327

VERSION

H99327.1

GI:1123995

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 358)

Reference

Authors

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 233

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert length: 2771 Std Error: 0.00

Seq primer: ml3 -40 forward

High quality sequence stop: 233.

FEATURES

source

1..358

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3872202"

/db\_xref="taxon:9606"

/clone="IMAGE:262560"

/sex="Male"

/tissue\_type="melanocyte"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares melanocyte 2NBM"

/note="Vector: pT7T3D (Pharmacia) with a modified

polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGGAGCGCGGAGTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library constructed by Bento Soares and  
M. Fatima Bonaldo. RNA from normal foreskin melanocytes  
(FS374) was kindly provided by Dr. Anthony P. Albino."

## ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 358;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGGTGGGCAACACAT 20

|||||

Db 163 GCTTGGTGGGCAACACAT 182

## RESULT 17

AI846721

LOCUS

DEFINITION

UI-M-AN1-afi-h-10-0-UI.s1 NIH BMAP MBG N Mus musculus cDNA clone  
UI-M-AN1-afi-h-10-0-UI 3', mRNA sequence.

ACCESSION

AI846721

VERSION

AI846721.1

GI:5490627

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 361)

Reference

Authors

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

8889548

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to verify it as a clone from the

normalized basal ganglia library cDNA Library Preparation: M.B.

Soares Lab Clone distribution: NIH BMAP cDNA clones will be made

available by the means that is soon to be determined. When NIH

determines the means for distribution of the BMAP cDNA clones, this

record will be updated accordingly when that means is determined.

The following repetitive elements were found in this cDNA sequence:

1-21, >AT-rich#Low\_complexity

Seq primer: M13 Forward

POLYA=Yes.

FEATURES

source

1..361

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UI-M-AN1-afi-h-10-0-UI"

/dev\_stage="27-32 days"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NIH BMAP MBG N"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not 1; Site 2: Eco RI; The

NIH BMAP MBG N library is a normalized library constructed

from mouse basal ganglia. The tag is a string of 5

nucleotides present between the Not I site and the

oligo-dT track. The library was constructed as described

by Bonaldo, Lennon and Soares, Genome Research 6:  
791-806, 1996. Tissue provided by Ms. Annie Novakovich,  
Zivic-Miller Laboratories.  
TAG TISSUE=basal-ganglia  
TAG\_L1B=NIH BMAP\_MBG\_N  
TAG\_SEQ=GTGAC

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 361;  
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0;

Qy 1 GCTTTGGTGGCAACACAT 20  
|||||

Db 173 GCTTTGGTGGCAACACAT 192  
|||||

RESULT 18  
AA035406  
LOCUS  
DEFINITION  
IMAGE:471713 3' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3  
(HUMAN);, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AA035406.1 GI:1507063  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 382)  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,  
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,  
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,  
Roifling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,  
Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.  
and Marra, M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)

TITLE  
JOURNAL  
PUBMED  
COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 902 Std Error: 0.00  
Seq primer: -40M13 fwd. from Amersham  
High quality sequence stop: 192.  
Location/Qualifiers  
1. .382  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:3757715"  
/db\_xref="taxon:9606"  
/clone="IMAGE:471713"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_pregnant uterus NBHPU"  
/note="Organ: uterus; Vector: pT7T3-Pac; Site:1: Not 1;  
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -  
oligo(dT) primer [5',  
AACTGGAGAAATTCGCGCCCTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization. Library  
constructed by M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 382;  
Best Local Similarity 100.0%; Pred. No. 0.31; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0;

Qy 1 GCTTTGGTGGCAACACAT 20  
|||||

Db 159 GCTTTGGTGGCAACACAT 178  
|||||

RESULT 19  
AW274010  
LOCUS  
DEFINITION  
IMAGE:2814248 3' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3  
(HUMAN);, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AW274010.1 GI:6661040  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 388)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -40UP from Gibco.  
Location/Qualifiers  
1. .388  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2814248"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL19W, testis NHT, and B-cell  
NCI-CGAP-GCB1) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 582632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 388;  
Best Local Similarity 100.0%; Pred. No. 0.31; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0;

Qy 1 GCTTTGGTGGCAACACAT 20  
|||||

Db 162 GCTTTGGTGGCAACACAT 181  
|||||

RESULT 20  
AA981734  
LOCUS  
DEFINITION  
IMAGE:1348288 5' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3  
(HUMAN);, mRNA sequence.

ACCESSION  
AA981734  
LOCUS  
DEFINITION  
IMAGE:1348288 5' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3  
(HUMAN);, mRNA sequence.



```

VERSION
KEYWORDS
SOURCE
ORGANISM

AA981734.1 GI:3160503
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geiseli,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE
The WashU-HMI Mouse EST Project

JOURNAL
Unpublished (1996)

COMMENT
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNLML; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:697080
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 173.
Location/Qualifiers
1..393
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1348288"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary_gland_NBMNG"
/note="Organ: mammary gland; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
TGTACCAATCTGAGTGGAGCGCCGCGAATGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAACACAT 20
|||||
Db 158 GCTTTGGTTGGCAACACAT 177

RESULT 21
AK212379/c
LOCUS
DEFINITION
Mus musculus cDNA, clone:Y2G0124M02, strand:minus.
reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000053764, based
on BLAT search.
ACCESSION
AK212379
VERSION
AK212379.1 GI:56036556
KEYWORDS
HTC; ASSETS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AA981734.1 GI:3160503
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Watahiki,A., Waki,K., Hayatsu,N., Shiraki,T., Kondo,S.,
Nakamura,M., Sasaki,D., Arakawa,T., Kawai,J., Harbers,M.,
Hayashizaki,Y. and Carninci,P.
Libraries enriched for alternatively spliced exons reveal splicing
patterns in melanocytes and melanomas
Nat. Methods 1, 233-239 (2004)
2 (bases 1 to 396)

AUTHORS
Arakawa,T., Carninci,P., Fukuda,S., Harbers,M., Hayatsu,N.,
Hori,F., Imotani,K., Kawai,J., Kondo,S., Murata,M., Nakamura,M.,
Nomura,K., Ohno,M., Sasaki,D., Shiraki,T., Waki,K., Watahiki,A. and
Hayashizaki,Y.

TITLE
Direct Submision

JOURNAL
Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Shiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT
Alternative Splicing Libraries (ASLs) are prepared by: Preparing
of single-stranded DNA using a RNA template from full length cDNA
libraries, hybridizing of
single-stranded DNAs, removing of remaining single-stranded DNA,
digesting of regions comprising double-stranded DNA by a set of 4
bp-cutters, capturing of DNA hybrids with loop structures
(alternative spliced exon), ligating of Y-shaped primers to
isolated DNA hybrids with loop structures, PCR amplification of
ligation products and their cloning into pFLCI vector. (Reference).
Location/Qualifiers
1..396
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="Y2G0124M02"
/cell_lines="mixture of B16-F10Y and melan-c"
/cell_type="mixture of melanoma cell and melanocyte cell"
/clone_lib="Alternative Splicing Library L3"
/note="strand:minus, reference:ENSEMBL:Mouse-Transcript-
ENST:ENSMUST0000053764, based on BLAT search"

ORIGIN
Query Match 100.0%; Score 20; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAACACAT 20
|||||
Db 230 GCTTTGGTTGGCAACACAT 211

RESULT 22
CF356230/c
LOCUS
DEFINITION
musculus cDNA clone IMAGE:6925620 5' similar to TR:Q9WVH5 Q9WVH5
FORKHEAD PROTEIN FKHL1. [1] ; mRNA sequence.
ACCESSION
CF356230
VERSION
CF356230.1 GI:34023168
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 396)
McCarrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Pape,D.,
Martin,J., Wylie,T., Dante,M., Bowers,Y., Theising,B., Gibbons,M.,
Ritter,E., Tsagareishvili,R., Ronko,I., Maguire,L., Kennedy,S.,
Bennett,J., Waterston,R. and Wilson,R.

TITLE
NIHES Mouse

```

JOURNAL  
COMMENT

Unpublished (2002)  
Contact: McCarrey/Eddy NIEHS Mouse  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Library constructed and donated by J. McCarrey, Ph.D. (Southwest  
Foundation for Biomedical Research, Dept. of Genetics) - excision  
done by E.M. Eddy, Ph.D. (National Institutes of Health, National  
Institute of Environmental Health Sciences).  
Seq primer: Primer name ambiguous.

## FEATURES

source

```
1. .396
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6925620"
/sex="male"
/tissue_type="6-day primitive type A spermatogonia"
/lab_host="DH10B (phage-resistant)"
/clone_lib="McCarrey Eddy 6 day primitive type A
spermatogonia"
/note="Organ: testis; Vector: pBluescript SK+
(Stratagene); Site 1: EcoRI; Site 2: XhoII; cDNA oligo
dt-primed [5'-(GA)10-ACTAGTCTCGAGTGTGTTT-3'] and
directionally cloned using 5' linkers 5'-AATTGGCGCAGG-3'
and 5'-CTCGTGGCG-3'. Size selection of >400bp material
gives average insert size ranging from 1-2 Kb. Library was
single-stranded phagemids were prepped and transformed into
DH10B. Library constructed and donated by J. McCarrey,
Ph.D. (Southwest Foundation for Biomedical Research, Dept.
of Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences)."
```

## ORIGIN

```
Query Match      100.0%; Score 20; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

## Qy

1 GCTTTGGTTGGCAACACAT 20

## Db

241 GCTTTGGTTGGCAACACAT 222

## RESULT 23

BP755053

## LOCUS

```
DEFINITION BP755053 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial9094 3',
mRNA sequence.
```

## ACCESSION

BP755053

## VERSION

BP755053.1 GI:50074943

## KEYWORDS

EST.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 397)

## AUTHORS

Nishimura, M., Yokoi, N., Miki, T., Horikawa, Y., Yoshioka, H.,  
Takeda, J., Ohara, O. and Seino, S.

## TITLE

Construction of a multi-functional cDNA library specific for mouse  
pancreatic islets and its application to microarray

## JOURNAL

DNA Res. 11 (5), 315-323 (2004)

## PUBMED

15747579

## COMMENT

Contact: Susumu Seino  
Division of Cellular and Molecular Medicine  
Kobe University Graduate School of Medicine  
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan

## FEATURES

source

```
1. .397
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="mial9094"
/sex="male"
/tissue_type="pancreatic islet"
/dev_stage="adult"
/clone_lib="mouse (C57BL/6) pancreatic islet library with
recombination-based method"
```

## ORIGIN

```
Query Match      100.0%; Score 20; DB 3; Length 397;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

## Qy

1 GCTTTGGTTGGCAACACAT 20

## Db

156 GCTTTGGTTGGCAACACAT 175

## RESULT 24

BY367902/c

## LOCUS

```
DEFINITION BY367902 RIKEN full-length enriched, 6 days neonate spleen Mus
musculus cDNA clone F420013K03 3', mRNA sequence.
```

## ACCESSION

BY367902

## VERSION

BY367902.1 GI:26597390

## KEYWORDS

EST.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 397)

## AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,  
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,  
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,  
Chothia, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A.,  
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,  
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,  
Kawaji, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Kongsawa, A.,  
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,  
Maltais, K., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,  
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,  
Ravasi, T., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,  
Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,  
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tonita, M.,  
Vardaro, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,  
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Haehizume, W., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs

## JOURNAL

Nature 420, 563-573 (2002)

## PUBMED

12466851

## COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic

Tel: 81-78-382-5360

Fax: 81-78-382-5370

Email: seino@med.kobe-u.ac.jp.

Location/Qualifiers

1. .397

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="mial9094"

/sex="male"

/tissue\_type="pancreatic islet"

/dev\_stage="adult"

/clone\_lib="mouse (C57BL/6) pancreatic islet library with  
recombination-based method"

Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H.,  
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, K.,  
Ohno, M., Saka, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
further details.

#### FEATURES

source

1..397

/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="F420013K03"  
/tissue\_type="spleen"  
/dev\_stage="6 days neonate"  
/clone\_lib="RIKEN full-length enriched, 6 days neonate  
spleen"

#### ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 397;

Best Local Similarity 100.0%; Pred. No. 0.31;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTGGGCAACACAT 20

Db 237 GCTTTGGTGGGCAACACAT 218

#### RESULT 25

AK211466/c

LOCUS AK211466 398 bp mRNA linear HTC 23-NOV-2004  
DEFINITION Mus musculus cDNA, clone:Y2G0121N15, strand:plus,  
reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000053764, based  
on BLAT search.

ACCESSION AK211466

VERSION AK211466.1 GI:56035643

KEYWORDS HTC; ASSETS.

SOURCE Mus musculus (house mouse)

#### ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE

AUTHORS

Watahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S.,  
Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M.,  
Hayashizaki, Y. and Carninci, P.  
Libraries enriched for alternatively spliced exons reveal splicing  
patterns in melanocytes and melanomas  
Nat. Methods 1, 233-239 (2004)

#### REFERENCE

AUTHORS

2 (bases 1 to 398)  
Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N.,  
Hori, F., Imotani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M.,  
Nomura, K., Ohno, M., Sasaki, D., Shiraki, T., Waki, K., Watahiki, A. and  
Hayashizaki, Y.

#### TITLE

JOURNAL

Direct Submission  
Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa, 230-0045, Japan [E-mail: genome-res@sc.riken.jp,  
URL: <http://genome.gsc.riken.jp>, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216]

#### COMMENT

Alternative Splicing Libraries (ASLs) are prepared by: Preparing  
of single-stranded DNA using a RNA template from full length cDNA  
libraries, hybridizing of  
single-stranded DNAs, removing of remaining single-stranded DNA,  
digesting of regions comprising double-stranded DNA by a set of 4  
bp-cutters, capturing of DNA hybrids with loop structures  
(alternative spliced exon), ligating of Y-shaped primers to  
isolated DNA hybrids with loop structures, PCR amplification of  
ligation products and their cloning into pFLCI vector. (Reference).

#### FEATURES

source

1..398

/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="Y2G0121N15"  
/cell\_lines="mixture of B16-F10Y and melan-c"  
/cell\_type="mixture of melanoma cell and melanocyte cell"  
/clone\_lib="Alternative Splicing Library L3"  
/note="strand:plus, reference:ENSEMBL:Mouse-Transcript-  
ENST:ENSMUST0000053764, based on BLAT search"

#### ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 398;

Best Local Similarity 100.0%; Pred. No. 0.31;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTGGGCAACACAT 20

Db 261 GCTTTGGTGGGCAACACAT 242

#### RESULT 26

BI401999

LOCUS

DEFINITION BI401999 403 bp mRNA linear EST 14-AUG-2001  
MI-P-CP0-nvu-d-11-0-UI s1 MI-P-CP0 Sus scrofa cDNA clone  
MI-P-CP0-nvu-d-11-0-UI 3', mRNA sequence.

ACCESSION BI401999

VERSION BI401999.1 GI:15181060

KEYWORDS EST.

SOURCE Sus scrofa (pig)

#### ORGANISM

Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.

#### REFERENCE

AUTHORS

TITLE

1 (bases 1 to 403)  
Ronald, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)

#### JOURNAL

PUBMED

COMMENT

Contact: Tuggle CK  
Molecular Genetics Laboratory, Department of Animal Science  
Iowa State University  
201 Klidde Hall, Ames, IA 50011-3150, USA  
Tel: 5152944252  
Fax: 5152942401  
Email: [ckugle@iastate.edu](mailto:ckugle@iastate.edu)

The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized uterus library cDNA library preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through Research Genetics (www.regen.com) The following repetitive elements were found in this cDNA sequence: 1-21,  
>AT rich#Low complexity  
Seq primer: M13 Forward  
POLYA=Yes.

## FEATURES

source

Location/Qualifiers

```
1..403
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="MI-P-CP0-nvu-d-11-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_lib="MI-P-CP0"
/note="Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-CP0
library is derived from uterus. For a detailed description
of the library from which this clone was derived, please
visit our web site at http://pigest.genome.iaSTATE.edu/.
The procedure used to create this library has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996)
TAG TISSUE=uterus
TAG LIB=MI-P-CP0
TAG_SEQ=AGTCCATCG"
```

## ORIGIN

```
Query Match      100.0%; Score 20; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20
|||||
Db 178 GCTTTGGTTGGCAACACAT 197
```

## RESULT 27

BB700991/c

LOCUS

```
DEFINITION BB700991 RIKEN full-length enriched, in vitro fertilized eggs Mus
musculus cDNA clone 7420426B07 3', mRNA sequence.
```

ACCESSION

BB700991

VERSION

BB700991.1

KEYWORDS

GI:16049815

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 404)

Akimura,T., Arawaka,T., Carninci,P., Furuno,M., Hanagaki,T.,

Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Imotani,K.,

Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,

Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,

Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,

Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,

Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akai,S.,

Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,

Muramatsu,M. and Hayashizaki,Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.

2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,  
Matsuyama,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.  
and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,  
Sugahara,Y. and Hayashizaki,Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
e mouse tissues.

## FEATURES

source

Location/Qualifiers

```
1..404
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="7420426B07"
/sex="female"
/tissue_type="in vitro fertilized eggs"
/dev_stage="egg"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, in vitro
fertilized eggs"
/note="Site 1: Sall; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'-
GAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
amplified by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'-
GAGAGAGATCTCGATTATTAATTAATCCCTCCCTCCCTCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI"
```

## ORIGIN

```
Query Match      100.0%; Score 20; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20
|||||
Db 249 GCTTTGGTTGGCAACACAT 230
```

## RESULT 28

BB835762/c

LOCUS

```
DEFINITION BB835762 RIKEN full-length enriched, mammary gland RCB-0527
Jyg-MC(B) cDNA Mus musculus cDNA clone G930038L06 3', mRNA
sequence.
```

ACCESSION

BB835762

VERSION

BB835762.1

KEYWORDS

GI:17014005

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



```
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through L1NL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:614340
Putative full length read
vector to vector length is 419
High quality sequence stop: 378.

FEATURES
source
1. 414
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:1125004"
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
/clone_lib="Knowles Solter mouse 2 cell"
/notes="Organ: embryo; Vector: pBluescribe (modified);
Site 1: MluI; Site 2: SalI; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
SalI (5'-CGGTCGACCGTCGACCGTTTCTTTT-3'.. cDNAs
were cloned into the MluI/SalI sites of a modified
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."

ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20
|||||
Db 262 GCTTTGGTTGGCAACACAT 243
|||||

RESULT 31
AJ647314/c 414 bp mRNA linear EST 07-JUL-2004
LOCUS
DEFINITION
AJ647314 CSEQRAN19 Sus scrofa cDNA clone C0003105_F08, mRNA
sequence.
ACCESSION
AJ647314 GI:49324159
VERSION
AJ647314.1
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 414)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(KS) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13p Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.ark-genomics.org.
Location/Qualifiers
1. 414

FEATURES
source
1. 414
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0003105_F08"
/tissue_type="ovary"
/clone_lib="CSEQRAN19"
/notes="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing; Normalised library
constructed from pooled ovaries"

ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20
|||||
Db 373 GCTTTGGTTGGCAACACAT 354
|||||

RESULT 32
AW825094 418 bp mRNA linear EST 17-MAY-2000
LOCUS
DEFINITION
AW825094.y1 Soares_NWGC B-cell Mus musculus cDNA clone
IMAGE:3166712 5' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3
(HUMAN); mRNA sequence.
ACCESSION
AW825094
VERSION
AW825094.1 GI:7918171
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 418)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MGI:1062172
Seq primer: -40RP from Gibco
High quality sequence stop: 393.
Location/Qualifiers
1. 418
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3166712"
/tissue_type="germinal B-cell from resting spleen"
/lab_host="DH10B (phage resistant)"
/clone_lib="Soares_NWGC B-cell"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA
was primed with a Not I.. oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGCAGATTCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 418;
```

```

Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAACACAT 20
Db 101 GCTTTGGTTGGCAACACAT 120

RESULT 33
BG230242
LOCUS
DEFINITION
IMAGE:3384926 3', similar to TR:Q9WVH5 Q9WVH5 FORKHEAD PROTEIN
FKH1. [1] ;, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 423)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG11089922
High quality sequence stop: 292.
Location/Qualifiers
1..423
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3384926"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Soares mouse NMGB bcell"
/clone_lib="Soares mouse NMGB bcell"
/Note="Organ: germinal B-cell; Vector: pRTT3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGCCGCTGTTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRTT3 vector.
Library is normalized; constructed by Bento Soares and
M.Fatima Bonaldo."
ORIGIN
Query Match 100.0%; Score 20; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAACACAT 20
Db 169 GCTTTGGTTGGCAACACAT 188

RESULT 34
BB828031/c
LOCUS
DEFINITION
JYG-MC(A) cDNA Mus musculus cDNA clone G830050G14 3', mRNA
425 bp mRNA linear EST 19-NOV-2001
BB828031
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
Mus musculus

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 425)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,P., Takaku-Akahira,S.,
Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-rs@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
Location/Qualifiers
1..425
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="G830050G14"
/tissue type="mammary gland"
/cell_line="RCB-0526 Jyg-MC(A)"
/clone_lib="RIKEN full-length enriched, mammary gland
RCB-0526 Jyg-MC(A) cDNA"
ORIGIN
Query Match 100.0%; Score 20; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAACACAT 20
Db 268 GCTTTGGTTGGCAACACAT 249

RESULT 35
CF138380/c
LOCUS
DEFINITION
UI-HF-BN0-aos-d-02-0-UI.r1 NIH MGC_50 Homo sapiens cDNA clone
IMAGE:3094658 5', mRNA sequence.
426 bp mRNA linear EST 09-SEP-2003
CF138380
ACCESSION
VERSION
KEYWORDS
CF138380.1 GI:33253824
EST.

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SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
REFERENCE   1 (bases 1 to 426)
AUTHORS    Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE      Normalization and subtraction: two approaches to facilitate gene
JOURNAL    Genome Res. 6 (9), 791-806 (1996)
PUBMED     889548
COMMENT    Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Louis Staudt
            cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/humanfl.html
            Seq primer: pYX-5.

FEATURES   source
            Location/Qualifiers
                1..426
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3094659"
                /tissue_type="lymph"
                /cell_type="germinal center B cells"
                /cell_line="MGC85"
                /lab_hosts="DH10B (LTI)"
                /clone_lib="NIH MGC 50"
                /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
                Constructed from size fractionated cytoplasmic mRNA
                (3.5-4.4kb). Directionally cloned. Cells provided by
                Louis M. Staudt, Ph.D. Library preparation by Maria de
                Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAACACAT 20
    |||||
Db 328 GCTTTGGTTGGGCAACACAT 309

RESULT 36
AA893671/c
LOCUS      AA893671
DEFINITION EST197474 Normalized rat placenta, Bento Soares Rattus sp. cDNA
            clone RPLA127 3' end, mRNA sequence.
ACCESSION  AA893671
VERSION     AA893671.1 GI:4132319
KEYWORDS   EST.
SOURCE      Rattus sp.
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidae; Muridae; Murinae; Rattus.
REFERENCE   1 (bases 1 to 427)
AUTHORS    Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
            Kerlavage,A.R. and Adams,M.D.
TITLE      Rat Genome Project: Generation of a Rat EST (RESt) Catalog & Rat
            Gene Index
JOURNAL    Unpublished (1998)
COMMENT    On Apr 3, 1998 this sequence version replaced gi:3020550.
            Contact: Lee, NH

SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Catarrhini;
            Homiidae; Homo.
REFERENCE   1 (bases 1 to 427)
AUTHORS    The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhlee@tigr.org
            Seq primer: M13-21.
            Location/Qualifiers
                1..427
                /organism="Rattus sp."
                /mol_type="mRNA"
                /db_xref="taxon:10118"
                /clone="RPLA127"
                /clone_lib="Normalized rat placenta, Bento Soares"
                /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
                Site_2: NotI"

ORIGIN
Query Match      100.0%; Score 20; DB 1; Length 427;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAACACAT 20
    |||||
Db 262 GCTTTGGTTGGGCAACACAT 243

RESULT 37
AA124874
LOCUS      AA124874
DEFINITION mp73508.r1 Soares thymus_2NDMT Mus musculus cDNA clone IMAGE:574862
            5', similar to gb:U02368 PAIRED BOX PROTEIN PAX-3 (HUMAN);, mRNA
            sequence.
ACCESSION  AA124874
VERSION     AA124874.1 GI:1684049
KEYWORDS   EST.
SOURCE      Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 427)
AUTHORS    Marra,M., Hillier,D., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
            The WashU-HMMI Mouse EST Project
            Unpublished (1996)
            Contact: Marra M/Mouse EST Project
            WashU-HMMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:349510
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 231.
            Location/Qualifiers
                1..427
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:574862"
                /sex="male"
                /tissue_type="Thymus"
                /dev_stage="4 weeks"
                /lab_hosts="DH10B"
                /clone_lib="Soares thymus_2NDMT"
                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified

```

rounds of normalization, and Soares and M. Fatima Bonaldo."

```
Query Match      100.0%; Score 20; DB 2; Length 433;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Accession	Gene	Size (bp)	Library	EST
U05677	OCUS	434	mRNA	linear
U05678	OCUS	434	mRNA	linear
U05679	OCUS	434	mRNA	linear
U05680	OCUS	434	mRNA	linear
U05681	OCUS	434	mRNA	linear
U05682	OCUS	434	mRNA	linear
U05683	OCUS	434	mRNA	linear
U05684	OCUS	434	mRNA	linear
U05685	OCUS	434	mRNA	linear
U05686	OCUS	434	mRNA	linear
U05687	OCUS	434	mRNA	linear
U05688	OCUS	434	mRNA	linear
U05689	OCUS	434	mRNA	linear
U05690	OCUS	434	mRNA	linear
U05691	OCUS	434	mRNA	linear
U05692	OCUS	434	mRNA	linear
U05693	OCUS	434	mRNA	linear
U05694	OCUS	434	mRNA	linear
U05695	OCUS	434	mRNA	linear
U05696	OCUS	434	mRNA	linear
U05697	OCUS	434	mRNA	linear
U05698	OCUS	434	mRNA	linear
U05699	OCUS	434	mRNA	linear
U05700	OCUS	434	mRNA	linear
U05701	OCUS	434	mRNA	linear
U05702	OCUS	434	mRNA	linear
U05703	OCUS	434	mRNA	linear
U05704	OCUS	434	mRNA	linear
U05705	OCUS	434	mRNA	linear
U05706	OCUS	434	mRNA	linear
U05707	OCUS	434	mRNA	linear
U05708	OCUS	434	mRNA	linear
U05709	OCUS	434	mRNA	linear
U05710	OCUS	434	mRNA	linear
U05711	OCUS	434	mRNA	linear
U05712	OCUS	434	mRNA	linear
U05713	OCUS	434	mRNA	linear
U05714	OCUS	434	mRNA	linear
U05715	OCUS	434	mRNA	linear
U05716	OCUS	434	mRNA	linear
U05717	OCUS	434	mRNA	linear
U05718	OCUS	434	mRNA	linear
U05719	OCUS	434	mRNA	linear
U05720	OCUS	434	mRNA	linear
U05721	OCUS	434	mRNA	linear
U05722	OCUS	434	mRNA	linear
U05723	OCUS	434	mRNA	linear
U05724	OCUS	434	mRNA	linear
U05725	OCUS	434	mRNA	linear
U05726	OCUS	434	mRNA	linear
U05727	OCUS	434	mRNA	linear
U05728	OCUS	434	mRNA	linear
U05729	OCUS	434	mRNA	linear
U05730	OCUS	434	mRNA	linear
U05731	OCUS	434	mRNA	linear
U05732	OCUS	434	mRNA	linear
U05733	OCUS	434	mRNA	linear
U05734	OCUS	434	mRNA	linear
U05735	OCUS	434	mRNA	linear
U05736	OCUS	434	mRNA	linear
U05737	OCUS	434	mRNA	linear
U05738	OCUS	434	mRNA	linear
U05739	OCUS	434	mRNA	linear
U05740	OCUS	434	mRNA	linear
U05741	OCUS	434	mRNA	linear
U05742	OCUS	434	mRNA	linear
U05743	OCUS	434	mRNA	linear
U05744	OCUS	434	mRNA	linear
U05745	OCUS	434	mRNA	linear
U05746	OCUS	434	mRNA	linear
U05747	OCUS	434	mRNA	linear
U05748	OCUS	434	mRNA	linear
U05749	OCUS	434	mRNA	linear
U05750	OCUS	434	mRNA	linear
U05751	OCUS	434	mRNA	linear
U05752	OCUS	434	mRNA	linear
U05753	OCUS	434	mRNA	linear
U05754	OCUS	434	mRNA	linear
U05755	OCUS	434	mRNA	linear
U05756	OCUS	434	mRNA	linear
U05757	OCUS	434	mRNA	

SYNOPSIS  
EST. 1954  
Mus musculus (house mouse)  
Mus musculus  
OPCANTISM

Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Mus musculus

Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 434)

Authors	Title
Piao, Y., Kargul, G.J., Budekula, D.B., Qian, Y., Luo, A., Carter, M.G., Umezawa, A. and Ko, M.S.H.	Systematic Analyses of NIA Mouse Mesenchymal Stem Cell cDNA Library

**JOURNAL**  
(long)  
Unpublished (2001)

Other ESTs: K0417G10-3  
Contact: Dawood B. Dudekula  
Department of Genetics

**Laboratory of Genetics**  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: [cdna@igsun.grc.nia.nih.gov](mailto:cdna@igsun.grc.nia.nih.gov)  
Plate: K0417 row: G column: 10

Seq primer: M13 Reverse  
High quality sequence stop: 434

FEATURES	
FOLIA=NO.	Location/Qualifiers
source	1. .434

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/organism="Mus musculus"  
/mol_type="mRNA"
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/strain="C3H/He"
/db_xref="nlcst:K0417G10-5N"
/db_xref="tacyon:10090"

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/u_xref:taxon:10050  
/clone="NIA:K0417G10 IMAGE:30060753"  
/tissue type="Mesenchymal stem cell"
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/tissue_type="Mesenchymal stem cell"
/cell_line="9-15-C cells"

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/lab_host="DH10B"
/clone_lib="NIA Mouse Mesenchymal Stem Cell cDNA Library"

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/clonotype_id="NIA Mouse Mesenchymal Stem Cell cDNA Library
(Long)"
(note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:

```

NotII; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research

Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 4: 573-579, 1994).

LI: 1553-1558 (2001). [PMID: 11544199]. Total RNAs were obtained from Dr. Akihiro Umezawa (Keio University School of Medicine, Japan). Double-stranded cDNAs were

of ribosomes), Japan; Bacterial Artificial Chromosomes were synthesized with an oligo(dT) primer (Invitrogen: 5'-pGACTAGTCTTAGATCGGAGCGCGCCCTTTTTTTTTTTT-3') from

2.2 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated

to lone-linker LL-Sa14, purified by phenol/chloroform, and

separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 434;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20  
|||||  
Db 65 GCTTTGGTTGGCAACACAT 46

RESULT 40  
AW912853  
LOCUS  
DEFINITION  
uf45912.y1 Soares mammary\_gland\_NMLMG Mus musculus linear EST 25-MAY-2000  
IMAGE:1514374 5' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3  
(HUMAN); mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AW912853  
AW912853.1 GI:8078479  
EST.  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

1 (bases 1 to 442)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:941226

Seq primer: -40RP from Gibco  
High quality sequence stop: 406.

## FEATURES

source  
Location/Qualifiers  
1..442  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1514374"  
/sex="female (lactating)"  
/tissue\_type="mammary gland"  
/lab\_host="DH10B"  
/clone\_lib="Soares mammary gland\_NMLMG"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from mammary  
gland tissue from a lactating female, and was then primed  
with a Not I - oligo (dr) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified pT73 vector. Library is normalized. Library  
was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 442;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20  
|||||

Db 132 GCTTTGGTTGGCAACACAT 151

## RESULT 41

AA280923  
LOCUS  
DEFINITION  
z997b12.r1 NCI\_CGAP GCB1 Homo sapiens cDNA clone IMAGE:711551 5',  
similar to gb:U02368 PAIRED BOX PROTEIN PAX-3 (HUMAN); mRNA  
sequence.

## ACCESSION

VERSION  
AA280923.1 GI:1923621

## KEYWORDS

SOURCE  
EST.

## ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1 (bases 1 to 447)

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 408.

## FEATURES

source

Location/Qualifiers  
1..447  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:711551"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP GCB1"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, IgD-),  
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo (dr) primer  
[5'-TGTTACCAATCTGACGTGGGCGGCGCTCAATTTTTTTTTTTT-3'  
]. Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 447;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20  
|||||

Db 159 GCTTTGGTTGGCAACACAT 178

## RESULT 42

AA897422  
LOCUS  
DEFINITION  
a148c09.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
IMAGE:1460560 3' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3  
(HUMAN); contains LTR1.b3 LTR1 repetitive element ; mRNA sequence.

## ACCESSION

VERSION  
AA897422.1 GI:3034042

## KEYWORDS

SOURCE  
EST.

## ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 448)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1331 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 443.
Location/Qualifiers
1..448
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1460560"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CCGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 448;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAACACAT 20
|||||
Db 160 GCTTTGGTTGGGCAACACAT 179

RESULT 43
BE849701 452 bp mRNA linear EST 26-SEP-2000
uw88all.y1 Soares mammary_gland NLMG Mus musculus cDNA clone
IMAGE:3469052 5' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3
(HUMAN); mRNA sequence.
BE849701
BE849701.1 GI:10308040
EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 452)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1388412
Seq primer: -40RP from Gibco
High quality sequence stop: 395.
Location/Qualifiers
1..452

```

```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 448)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1331 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 443.
Location/Qualifiers
1..448
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1460560"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CCGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 448;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAACACAT 20
|||||
Db 160 GCTTTGGTTGGGCAACACAT 179

RESULT 43
BE849701 452 bp mRNA linear EST 26-SEP-2000
uw88all.y1 Soares mammary_gland NLMG Mus musculus cDNA clone
IMAGE:3469052 5' similar to gb:U02368 PAIRED BOX PROTEIN PAX-3
(HUMAN); mRNA sequence.
BE849701
BE849701.1 GI:10308040
EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 452)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1388412
Seq primer: -40RP from Gibco
High quality sequence stop: 395.
Location/Qualifiers
1..452

```

BI294032 457 bp mRNA linear EST 19-JUL-2001  
LOCUS UI-R-DKO-cdy-e-08-0-UI\_s1 UI-R-DKO Rattus norvegicus cDNA clone  
DEFINITION UI-R-DKO-cdy-e-08-0-UI 3', mRNA sequence.  
ACCESSION BI294032  
VERSION BI294032.1 GI:14956100  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Rattus.  
1 (bases 1 to 457)  
REFERENCE Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
PUBMED 8889548  
COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEERF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. The sequence tag present in the cDNA between the NotI site  
and the oligo-dT track served to identify it as a clone from the  
normalized rat placenta pool library cDNA Library Preparation: M.B.  
Soares Lab Clone Distribution: clones will be available through  
Research Genetics (www.resgen.com) The following repetitive  
elements were found in this cDNA sequence: 1-21,  
>AT\_richLow complexity  
Seq primer: M13 Forward  
POLYA=yes.

FEATURES  
source

Location/Qualifiers  
1..457  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clones="UI-R-DKO-cdy-e-08-0-UI"  
/dev\_stage="ADULT"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-DKO"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-DKO  
library is a subtracted library derived from a mixture of  
five individually tagged normalized rat libraries:  
brain-nRBP (20%), heart-nRHP (20%), kidney-nRKP (20%),  
aorta-nRAP (20%), and placenta-nRPP (20%). Each original  
library was constructed from a mixture of equal amounts of  
RNA from seven different developmental time-points:  
embryonic day 17, embryonic day 19, embryonic day 21,  
adult day 1, adult day 12, adult day 75, and adult day  
200. (Exception: the aorta pool does not contain embryonic  
day 17 RNA and the placenta pool contains only the three  
embryonic stages). Each library was normalized  
individually according to the procedure described by  
Bonaldo, Lennon & Soares (Genome Research Genome 6:  
791-806, 1996). For construction of the DKO subtracted  
library, plasmid DNA from each of the five individually  
tagged normalized libraries was mixed in the proportions  
specified above and electroporated into competent bacteria  
for production of single-stranded circular DNA  
representing the pool of libraries. Single-stranded  
circular DNA representing these five normalized libraries  
was then used as a tracer in a subtractive hybridization  
with a driver (PCR amplified inserts from a plasmid DNA  
template preparation) comprising: a) a set of about 1,000  
arrayed clones from each of the five non-normalized

libraries of brain (CT0a), heart (CS0a), kidney (CU0a),  
aorta (CW0a), and placenta (CX0a). The resulting pool of  
approximately 5,000 clones represented about 33.3% of the  
final driver population. A set of about 2,000 arrayed  
clones from each of the five normalized libraries of brain  
(CT0), heart (CS0), kidney (CU0), aorta (CW0), and  
placenta (CX0). The resulting pool of about 10,000 clones  
represented about 66.6% of the final driver population.  
TAG TISSUE=rat placenta pool  
TAG LIB=UI-R-DKO  
TAG\_SEQ=TCACGACAGT"

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 457;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCTTTGGTTGGGCACACAT 20  
|||||  
Db 173 GCTTTGGTTGGGCACACAT 192

## RESULT 46

BI294032 461 bp mRNA linear EST 17-DEC-2003  
LOCUS H3065B05-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone  
DEFINITION H3065B05 3', mRNA sequence.  
ACCESSION BG068406  
VERSION BG068406.2 GI:40016024  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1 (bases 1 to 461)  
REFERENCE Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,  
Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H.,  
Wood,W.H., III, Becker,K.G. and Ko,M.S.H.  
TITLE Genome-wide expression profiling of mid-gestation placenta and  
embryo using a 15,000 mouse developmental cDNA microarray  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)  
PUBMED 10922068  
COMMENT On Jan 26, 2001 this sequence version replaced gi:12550975.  
Other ESTs: H3065B05-5  
Contact: George J. Kargul  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdaelgusn.grc.nia.nih.gov  
This clone set has been freely distributed to the community. Please  
visit <http://lgusun.grc.nia.nih.gov/cDNA/15k.html> for details.  
Plate: H3065 ROW: B column: 05  
Seq primer: -21M13 Forward  
High quality sequence stop: 461  
POLYA=yes.

FEATURES  
source

Location/Qualifiers  
1..461  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="niaEST:H3065B05-3"  
/db\_xref="taxon:10090"  
/clone="H3065B05"  
/sex="Clones arrayed from a variety of cDNA libraries"  
/dev\_stage="Clones arrayed from a variety of cDNA libraries"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse 15K cDNA Clone Set"  
/notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This  
clone is among a rearrayed set of 15,247 clones from 11  
embryo cDNA libraries (including preimplantation stage  
embryos from unfertilized egg to blastocyst, embryonic

part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, *Proc. Natl. Acad. Sci. U S A*, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, *Development*, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, *Hum Mol Genet* 7: 1967-1978."

## ORIGIN

```
Query Match      100.0%; Score 20; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GCTTTGGTTGGGCAACACAT 20  
156 GCTTTGGTTGGGCAACACAT 175

RESULT	47
AU022008	
LOCUS	
DEFINITION	AU022008 Mouse unfertilized egg cDNA Mus musculus cdna clone J0406P11 3', mRNA sequence.
ACCESSION	AU022008
VERSION	AU022008.1 GI:3386967
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 467)
AUTHORS	Ko,M.S.H., Kitchen,U.R., Wang,X., Threat,T.A., Sun,T., DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R. and Doi,H.
TITLE	Systemic analyses of genes expressed in unfertilized mouse eggs (The ERATO/Doi Project at Wayne State University) (Ko,M.S.H. et al.)

## ORIGIN

```
Query Match      100.0%; Score 20; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GCCTTGGTTGGCAACACAT 20  
|||  
Db 156 GCCTTGGTTGGCAACACAT 175

RESULT 48  
AI373959

LOCUS	AI373959	468 bp	mrna	linear	EST 16-FEB-1999
DEFINITION	Q951d1.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2041941 3', similar to gb:U02368 PAIRED BOX PROTEIN PAX-3 (HUMAN) ;, mRNA sequence.				
ACCESSION	AI373959				
VERSION	AI373959.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 468)				
AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapsb-r@mail.nih.gov">cgapsb-r@mail.nih.gov</a> This clone is available royalty-free through LNL ; contact the IMAGE Consortium ( <a href="mailto:info@image.lnl.gov">info@image.lnl.gov</a> ) for further information. Insert Length: 406 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 436.				

## ORIGIN

Query Match	100.0%;	Score 20;	DB 1;	Length 468;
Best Local Similarity	100.0%;	Pred. NO. 0.31;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 GCTTGGTTGGGCAACACAT 20  
Db 159 GCTTGGTTGGGCAACACAT 178

RESULT 49	BB702712/c	LOCUS	BB702712	471 bp	mRNA	linear	EST 11-OCT-2001
		DEFINITION	BB702712 RIKEN full-length enriched, in vitro fertilized eggs Mus musculus cDNA clone 7420443L11.3', mRNA sequence.				

Qy 1 GCCTTGGTTGGCAACACAT 20  
|||  
Db 156 GCCTTGGTTGGCAACACAT 175

Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,  
Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,  
Muramatsu,M. and Hayashizaki,Y.  
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.  
2001)

## TITLE

Unpublished (2001)

## JOURNAL

## COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,  
Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.  
and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,  
Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.

e mouse tissues.

## FEATURES

source

Location/Qualifiers

1. .471

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="7420443L11"

/sex="female"

/tissue\_type="in vitro fertilized eggs"

/dev\_stage="egg"

/lab\_host="DH10B"

/clone\_lib="RIKEN full-length enriched, in vitro

fertilized eggs"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5',  
GAGAGAGAGAGGATCAAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. Second strand cDNA was prepared with the  
primer adapter of sequence [5',  
GAGAGAGAGATTCGAGTTAATTAATTAATCCCCCCCCC 3']. cDNA  
was cloned into the XhoI and BamHI sites. Vector: a  
modified pBluescript KS(+) after bulk excision from Lambda  
FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 471;

Best Local Similarity 100.0%; Pred. No. 0.31;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20

|||||

Db 316 GCTTTGGTTGGCAACACAT 297

RESULT 50

BF388801

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa;

Mammalia; Eutheria;

Euarchontoglires;

Glires; Rodentia;

Sciurognathi;

Muroidea;

Muridae;

Rattus.

1 (bases 1 to 472)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to verify it as a clone from the

normalized embryo at 13 dpc library cDNA Library Preparation: M.B.

Soares Lab Clone distribution: clones will be available through

Research Genetics ([www.resgen.com](http://www.resgen.com))

Seq primer: M13 Forward

POLYA=Yes.

Location/Qualifiers

1. .472

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-BS2-bde-f-12-0-UI"

/dev\_stage="embryonic 13 dpc"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="UI-R-BS2"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BS2

library is a subcloned library derived from 13 dpc whole

embryo tissue. For a detailed description of the library

from which this clone was derived, please visit our web

site at [ratest.eng.uiowa.edu](http://ratest.eng.uiowa.edu). The subtraction has been

previously described in (Bonaldo, Lennon and Soares,

Genome Research 6:791-806, 1996)

TAG TISSUE=embryo at 13 dpc

TAG LIB=UI-R-BS2

TAG\_SEQ=AATCC"

## ORIGIN

Query Match

Best Local Similarity

Matches 20; Conservative

0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20

|||||

Db 172 GCTTTGGTTGGCAACACAT 191

Search completed: May 8, 2006, 02:26:04

Job time : 3834 secs



GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 00:50:50 ; Search time 427 Seconds  
(without alignments)  
190.751 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20

Sequence: 1 gcttgggtggcaacacat 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 9306428 seqs, 2036268586 residues

Word size : 1

Total number of hits satisfying chosen parameters: 18612072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications NA New:\*

- 1: /SIDSS/ptodata/1/pubpna/US08\_NEW\_PUB.seq1.\*
- 2: /SIDSS/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /SIDSS/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /SIDSS/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 5: /SIDSS/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 6: /SIDSS/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 7: /SIDSS/ptodata/1/pubpna/US09\_NEW\_PUB.seq1.\*
- 8: /SIDSS/ptodata/1/pubpna/US09\_NEW\_PUB.seq2.\*
- 9: /SIDSS/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 10: /SIDSS/ptodata/1/pubpna/US10\_NEW\_PUB.seq1.\*
- 11: /SIDSS/ptodata/1/pubpna/US10\_NEW\_PUB.seq2.\*
- 12: /SIDSS/ptodata/1/pubpna/US10\_NEW\_PUB.seq3.\*
- 13: /SIDSS/ptodata/1/pubpna/US10\_NEW\_PUB.seq4.\*
- 14: /SIDSS/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 15: /SIDSS/ptodata/1/pubpna/US11\_NEW\_PUB.seq1.\*
- 16: /SIDSS/ptodata/1/pubpna/US11\_NEW\_PUB.seq2.\*
- 17: /SIDSS/ptodata/1/pubpna/US11\_NEW\_PUB.seq3.\*
- 18: /SIDSS/ptodata/1/pubpna/US11\_NEW\_PUB.seq4.\*
- 19: /SIDSS/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Ref. No.	Score	Match	Length	ID	Description
1	20	100.0	25	17	US-11-136-527-226522
2	20	100.0	254	12	US-10-920-152-12
3	20	100.0	600	17	US-11-136-527-4790
4	20	100.0	1803	17	US-11-136-527-34023
5	20	100.0	3517	13	US-10-469-469-192
6	19	95.0	25	17	US-11-136-527-34022
7	19	95.0	25	17	US-11-136-527-226492
8	19	95.0	25	17	US-11-136-527-226494
9	18	90.0	25	17	US-11-136-527-34046
10	17	85.0	25	17	US-11-136-527-34023
11	16	80.0	25	17	US-11-136-527-34042
12	16	80.0	995	12	US-10-301-480-546810
13	16	80.0	995	12	US-10-301-480-1160219
14	16	80.0	996	12	US-10-301-480-553142

Sequence 553488,	12	US-10-301-480-553488	996	12	80.0	16	C 15
Sequence 1166551,	12	US-10-301-480-1166551	996	12	80.0	16	C 16
Sequence 1166897,	12	US-10-301-480-1166897	996	12	80.0	16	C 17
Sequence 34024, A	25	US-11-136-527-34024	25	17	75.0	15	C 18
Sequence 541667,	1000	US-10-301-480-541667	1000	12	75.0	15	C 19
Sequence 1155076,	1000	US-10-301-480-1155076	1000	12	75.0	15	C 20
Sequence 669805,	7	US-09-925-065A-669805	1153	7	75.0	15	C 21
Sequence 22, Appl	3593	US-10-115-609-22	3593	11	75.0	15	C 22
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Sequence 25760, A	201	US-11-124-367A-25760	201	17	70.0	14	C 24
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Sequence 247396,	404	US-10-301-480-247396	404	12	70.0	14	C 26
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Sequence 14320, A	468	US-10-301-480-14320	468	11	70.0	14	C 28
Sequence 627729,	468	US-10-301-480-627729	468	12	70.0	14	C 29
Sequence 603534,	506	US-09-925-065A-603534	506	7	70.0	14	C 30
Sequence 603533,	515	US-09-925-065A-603533	515	7	70.0	14	C 31
Sequence 425083,	535	US-10-301-480-425083	535	12	70.0	14	C 32
Sequence 425084,	535	US-10-301-480-425084	535	12	70.0	14	C 33
Sequence 425085,	535	US-10-301-480-425085	535	12	70.0	14	C 34
Sequence 1038493,	535	US-10-301-480-1038493	535	12	70.0	14	C 35
Sequence 1038494,	535	US-10-301-480-1038494	535	12	70.0	14	C 36
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Sequence 803178,	545	US-10-301-480-803178	545	12	70.0	14	C 43
Sequence 415497,	556	US-10-301-480-415497	556	12	70.0	14	C 44
Sequence 415498,	556	US-10-301-480-415498	556	12	70.0	14	C 45
Sequence 1028906,	556	US-10-301-480-1028906	556	12	70.0	14	C 46
Sequence 1028907,	556	US-10-301-480-1028907	556	12	70.0	14	C 47
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Sequence 463577,	592	US-09-925-065A-463577	592	7	70.0	14	C 57
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Sequence 901609,	593	US-10-301-480-901609	593	12	70.0	14	C 60
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Sequence 1133458,	595	US-10-301-480-1133458	595	12	70.0	14	C 65
Sequence 1133459,	595	US-10-301-480-1133459	595	12	70.0	14	C 66
Sequence 1133460,	595	US-10-301-480-1133460	595	12	70.0	14	C 67
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Sequence 540729,	601	US-09-925-065A-540729	601	7	70.0	14	C 71
Sequence 902618,	602	US-09-925-065A-902618	602	7	70.0	14	C 72
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Sequence 536665,	998	US-10-301-480-536665	998	12	70.0	14	C 79
Sequence 1150074,	998	US-10-301-480-1150074	998	12	70.0	14	C 80
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c 88	14	70.0	1335	12	US-10-301-480-640819	Sequence 640819,	161	13	65.0	566	12	US-10-301-480-634114	Sequence 634114,
c 89	14	70.0	1335	12	US-10-301-480-640820	Sequence 640820,	162	13	65.0	588	7	US-09-925-065A-521903	Sequence 521903,
c 90	14	70.0	1335	12	US-10-301-480-640821	Sequence 640821,	163	13	65.0	588	12	US-10-301-480-408727	Sequence 408727,
c 91	14	70.0	1839	18	US-11-079-463-1731	Sequence 1731, Ap	164	13	65.0	588	12	US-10-301-480-1022136	Sequence 1022136,
c 92	14	70.0	1931	7	US-09-925-065A-723533	Sequence 723533,	165	13	65.0	590	7	US-09-925-065A-246451	Sequence 246451,
c 93	14	70.0	2196	7	US-09-925-065A-683172	Sequence 683172,	166	13	65.0	591	7	US-09-925-065A-648059	Sequence 648059,
c 94	14	70.0	2197	13	US-10-469-469-213	Sequence 213, App	c 167	13	65.0	591	7	US-09-925-065A-935924	Sequence 935924,
c 95	14	70.0	2197	13	US-10-469-469-215	Sequence 215, App	c 168	13	65.0	591	7	US-09-925-065A-935925	Sequence 935925,
c 96	14	70.0	2314	11	US-10-301-480-96382	Sequence 96382, A	c 169	13	65.0	592	7	US-09-925-065A-335272	Sequence 335272,
c 97	14	70.0	2314	11	US-10-301-480-96383	Sequence 96383, A	c 170	13	65.0	596	7	US-09-925-065A-754854	Sequence 754854,
c 98	14	70.0	2314	12	US-10-301-480-709791	Sequence 709791,	c 171	13	65.0	596	7	US-09-925-065A-754855	Sequence 754855,
c 99	14	70.0	2314	12	US-10-301-480-709792	Sequence 709792,	c 172	13	65.0	597	7	US-09-925-065A-825513	Sequence 825513,
c 100	14	70.0	2493	11	US-10-932-182A-78335	Sequence 78335, A	c 173	13	65.0	597	11	US-10-301-480-9010	Sequence 9010, Ap
c 101	14	70.0	2493	11	US-10-932-182A-78335	Sequence 78335, A	c 174	13	65.0	597	11	US-10-301-480-622419	Sequence 622419, Ap
c 102	14	70.0	3160	18	US-11-141-611-51	Sequence 51, Appl	c 175	13	65.0	600	10	US-10-750-185-2706	Sequence 2706, Ap
c 103	14	70.0	3256	7	US-09-925-065A-688254	Sequence 688254,	c 176	13	65.0	600	10	US-10-750-623-2706	Sequence 2706, Ap
c 104	14	70.0	52192	10	US-10-995-561-13231	Sequence 13231, A	c 177	13	65.0	609	7	US-09-925-065A-478182	Sequence 478182,
c 105	13	65.0	18	10	US-10-310-914A-171448	Sequence 171448,	c 178	13	65.0	609	7	US-09-925-065A-478183	Sequence 478183,
c 106	13	65.0	19	10	US-10-310-914A-1371526	Sequence 1371526,	c 179	13	65.0	609	11	US-10-301-480-58560	Sequence 58560, A
c 107	13	65.0	21	10	US-10-310-914A-171416	Sequence 171416,	c 180	13	65.0	609	11	US-10-301-480-58561	Sequence 58561, A
c 108	13	65.0	21	10	US-10-310-914A-791926	Sequence 791926,	c 181	13	65.0	609	12	US-10-301-480-671969	Sequence 671969,
c 109	13	65.0	22	10	US-10-310-914A-171417	Sequence 171417,	c 182	13	65.0	609	12	US-10-301-480-671970	Sequence 671970,
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c 112	13	65.0	23	10	US-10-310-914A-791830	Sequence 791830,	c 185	13	65.0	621	7	US-09-925-065A-481727	Sequence 481727,
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c 114	13	65.0	24	10	US-10-310-914A-1371594	Sequence 1371594,	c 187	13	65.0	624	11	US-10-932-182A-5628	Sequence 5628, Ap
c 115	13	65.0	25	11	US-10-932-182A-116229	Sequence 116229,	c 188	13	65.0	631	7	US-09-925-065A-411439	Sequence 411439,
c 116	13	65.0	25	11	US-10-932-182A-116229	Sequence 116229	c 189	13	65.0	638	7	US-09-925-065A-49102	Sequence 49102, A
c 117	13	65.0	25	11	US-10-934-048A-3168	Sequence 3168, Ap	c 190	13	65.0	638	11	US-10-301-480-150340	Sequence 150340, A
c 118	13	65.0	25	17	US-11-121-849-216127	Sequence 216127,	c 191	13	65.0	638	12	US-10-301-480-763749	Sequence 763749,
c 119	13	65.0	25	17	US-11-136-527-34009	Sequence 34009, A	c 192	13	65.0	640	12	US-10-301-480-763742	Sequence 763742,
c 120	13	65.0	25	17	US-11-136-527-226524	Sequence 226524,	c 193	13	65.0	640	12	US-10-301-480-1091056	Sequence 1091056,
c 121	13	65.0	201	10	US-10-995-561-50021	Sequence 50021, A	c 194	13	65.0	647	7	US-09-925-065A-512632	Sequence 512632,
c 122	13	65.0	377	7	US-09-925-065A-491370	Sequence 491370,	c 195	13	65.0	647	7	US-09-925-065A-512633	Sequence 512633,
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c 126	13	65.0	454	18	US-11-116-881A-213139	Sequence 2139, Ap	c 199	13	65.0	656	7	US-09-925-065A-771622	Sequence 771622,
c 127	13	65.0	506	17	US-11-128-061-6409	Sequence 6409, Ap	c 200	13	65.0	658	7	US-09-925-065A-882868	Sequence 882868,
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c 131	13	65.0	511	12	US-10-301-480-775069	Sequence 775069,	c 204	13	65.0	683	7	US-09-925-065A-79305	Sequence 79305, A
c 132	13	65.0	515	7	US-09-925-065A-590910	Sequence 590910,	c 205	13	65.0	683	11	US-10-301-480-180544	Sequence 180544,
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c 135	13	65.0	521	12	US-10-301-480-309528	Sequence 309528,	c 208	13	65.0	700	12	US-10-301-480-1164401	Sequence 1164401,
c 136	13	65.0	521	12	US-10-301-480-922937	Sequence 922937,	c 209	13	65.0	713	7	US-09-925-065A-82461	Sequence 82461, A
c 137	13	65.0	528	7	US-09-925-065A-224786	Sequence 224786,	c 210	13	65.0	713	11	US-10-301-480-183701	Sequence 183701,
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c 154	13	65.0	561	11	US-10-301-480-59681	Sequence 59681, A	c 227	13	65.0	788	11	US-10-301-480-170715	Sequence 170715,
c 155	13	65.0	561	12	US-10-301-480-673090	Sequence 673090,	c 228	13	65.0	788	12	US-10-301-480-784123	Sequence 784123,
c 156	13	65.0	563	11	US-10-301-480-196812	Sequence 196812,	c 229	13	65.0	788	12	US-10-301-480-784124	Sequence 784124,
c 157	13	65.0	563	11	US-10-301-480-196813	Sequence 196813,	c 230	13	65.0	788	12	US-10-301-480-784124	Sequence 784124,
c 158	13	65.0	563	12	US-10-301-480-810221	Sequence 810221,	c 231	13	65.0	794	10	US-10-750-185-55483	Sequence 55483, A
c 159	13	65.0	563	12	US-10-301-480-810222	Sequence 810222,	c 232	13	65.0	810	7	US-09-925-065A-86355	Sequence 86355, A
c 160	13	65.0	566	11	US-10-301-480-20705	Sequence 20705, A	c 233	13	65.0	810	11	US-10-301-480-187595	Sequence 187595,

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238	13	65.0	838	12	US-10-301-480-1214004	Sequence 1214004, A	311	13	65.0	2905	7	US-09-925-065A-712239	Sequence 712239, A
239	13	65.0	876	7	US-09-925-065A-715791	Sequence 715791, A	312	13	65.0	2905	7	US-09-925-065A-712240	Sequence 712240, A
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258	13	65.0	1118	11	US-10-301-480-173187	Sequence 173187, A	331	13	65.0	4190	17	US-11-091-883-430	Sequence 430, App
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262	13	65.0	1200	7	US-09-925-065A-2693	Sequence 2693, App	335	13	65.0	79329	11	US-10-330-773-483	Sequence 483, App
263	13	65.0	1200	11	US-10-301-480-103929	Sequence 103929, A	336	13	65.0	100000	17	US-11-124-367A-5027	Sequence 5027, App
264	13	65.0	1200	11	US-10-301-480-103930	Sequence 103930, A	337	13	65.0	160213	17	US-11-121-086-103	Sequence 103, App
265	13	65.0	1200	12	US-10-301-480-717338	Sequence 717338, A	338	13	65.0	185393	17	US-11-121-086-101	Sequence 101, App
266	13	65.0	1200	12	US-10-301-480-717339	Sequence 717339, A	339	13	65.0	197241	18	US-11-114-798-47	Sequence 47, Appli
267	13	65.0	1304	11	US-10-301-480-38178	Sequence 38178, A	340	13	65.0	201990	10	US-10-995-561-13303	Sequence 13303, A
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269	13	65.0	1369	10	US-10-750-185-63004	Sequence 63004, A	342	13	65.0	2944528	18	US-11-045-004-1	Sequence 1, Appli
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c 381	12	60.0	25	11	US-10-932-182A-150829	Sequence 150829, A	454	12	60.0	451	7	US-09-925-065A-536155	Sequence 536155,
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c 383	12	60.0	25	11	US-10-932-182A-150829	Sequence 150829, A	c 456	12	60.0	451	7	US-09-925-065A-555286	Sequence 555286,
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389	12	60.0	25	17	US-11-121-849-369773	Sequence 369773, A	c 463	12	60.0	455	7	US-09-925-065A-269825	Sequence 269825,
c 390	12	60.0	25	17	US-11-121-849-610569	Sequence 610569, A	c 464	12	60.0	457	7	US-09-925-065A-471320	Sequence 471320,
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c 394	12	60.0	25	17	US-11-121-849-616319	Sequence 616319, A	468	12	60.0	457	12	US-10-301-480-1003664	Sequence 1003664,
c 395	12	60.0	25	17	US-11-136-527-34008	Sequence 34008, A	469	12	60.0	459	7	US-09-925-065A-621852	Sequence 621852,
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c 397	12	60.0	25	17	US-11-136-527-245633	Sequence 245633, A	471	12	60.0	468	7	US-09-925-065A-434070	Sequence 434070,
c 398	12	60.0	27	10	US-10-310-914A-136891	Sequence 136891, A	c 472	12	60.0	468	12	US-10-301-480-347367	Sequence 347367,
c 399	12	60.0	38	18	US-11-148-280-34	Sequence 34, Appl	c 473	12	60.0	468	12	US-10-301-480-960776	Sequence 960776,
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c 402	12	60.0	70	10	US-10-310-914A-5287	Sequence 5287, Ap	c 476	12	60.0	472	18	US-11-096-568A-14159	Sequence 14159, A
c 403	12	60.0	74	10	US-10-310-914A-5287	Sequence 5287, Ap	c 477	12	60.0	472	18	US-11-251-226-1	Sequence 1, Appl
c 404	12	60.0	200	17	US-11-098-686-1553	Sequence 1553, Ap	478	12	60.0	475	7	US-09-925-065A-96552	Sequence 96552, A
c 405	12	60.0	200	17	US-11-098-686-7363	Sequence 7363, Ap	479	12	60.0	475	7	US-09-925-065A-96553	Sequence 96553, A
c 406	12	60.0	200	18	US-11-251-226-2	Sequence 2, Appl	c 480	12	60.0	475	7	US-09-925-065A-96554	Sequence 96554, A
c 407	12	60.0	201	10	US-10-995-561-28379	Sequence 28379, A	c 481	12	60.0	475	7	US-09-925-065A-504269	Sequence 504269,
c 408	12	60.0	201	10	US-10-995-561-28381	Sequence 28381, A	482	12	60.0	475	12	US-10-301-480-362593	Sequence 362593,
c 409	12	60.0	201	10	US-10-995-561-33001	Sequence 33001, A	483	12	60.0	475	12	US-10-301-480-976002	Sequence 976002,
c 410	12	60.0	201	10	US-10-995-561-33093	Sequence 33093, A	c 484	12	60.0	476	7	US-09-925-065A-765026	Sequence 765026,
c 411	12	60.0	201	10	US-10-995-561-33176	Sequence 33176, A	c 485	12	60.0	480	7	US-09-925-065A-578364	Sequence 578364,
c 412	12	60.0	201	10	US-10-995-561-41467	Sequence 41467, A	c 486	12	60.0	481	12	US-10-301-480-453112	Sequence 453112,
c 413	12	60.0	201	10	US-10-995-561-41468	Sequence 41468, A	c 487	12	60.0	481	12	US-10-301-480-1065521	Sequence 1065521,
c 414	12	60.0	201	10	US-10-995-561-47443	Sequence 47443, A	c 488	12	60.0	482	7	US-09-925-065A-384338	Sequence 384338,
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c 416	12	60.0	201	10	US-10-995-561-55138	Sequence 55138, A	490	12	60.0	484	12	US-10-301-480-496258	Sequence 496258,
c 417	12	60.0	201	10	US-10-995-561-57448	Sequence 57448, A	c 491	12	60.0	484	12	US-10-301-480-1109667	Sequence 1109667,
c 418	12	60.0	201	10	US-10-995-561-59078	Sequence 59078, A	c 492	12	60.0	485	12	US-10-301-480-313888	Sequence 313888,
c 419	12	60.0	201	10	US-10-995-561-67652	Sequence 67652, A	c 493	12	60.0	485	12	US-10-301-480-927297	Sequence 927297,
c 420	12	60.0	201	10	US-10-995-561-71628	Sequence 71628, A	494	12	60.0	487	7	US-09-925-065A-580966	Sequence 580966,
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c 422	12	60.0	201	17	US-11-124-368A-11226	Sequence 11226, A	c 496	12	60.0	487	12	US-10-301-480-99805	Sequence 99805,
c 423	12	60.0	201	17	US-11-124-368A-13139	Sequence 13139, A	c 497	12	60.0	487	12	US-10-301-480-99805	Sequence 99805,
c 424	12	60.0	201	17	US-11-124-368A-13202	Sequence 13202, A	c 498	12	60.0	489	11	US-10-301-480-59308	Sequence 59308, A
c 425	12	60.0	201	17	US-11-124-368A-18521	Sequence 18521, A	c 499	12	60.0	489	12	US-10-301-480-672039	Sequence 672039,
c 426	12	60.0	201	17	US-11-124-367A-9388	Sequence 9388, Ap	499	12	60.0	490	7	US-09-925-065A-818693	Sequence 818693,
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c 428	12	60.0	201	17	US-11-124-367A-17557	Sequence 17557, A	c 501	12	60.0	491	7	US-09-925-065A-230231	Sequence 230231,
c 429	12	60.0	201	17	US-11-124-367A-19654	Sequence 19654, A	c 502	12	60.0	491	7	US-09-925-065A-310969	Sequence 310969,
c 430	12	60.0	201	17	US-11-124-367A-19948	Sequence 19948, A	c 503	12	60.0	494	7	US-09-925-065A-731624	Sequence 731624,
c 431	12	60.0	201	17	US-11-124-367A-19949	Sequence 19949, A	c 504	12	60.0	495	7	US-09-925-065A-381138	Sequence 381138,
c 432	12	60.0	201	17	US-11-124-367A-20030	Sequence 20030, A	c 505	12	60.0	495	7	US-09-925-065A-381139	Sequence 381139,
c 433	12	60.0	201	17	US-11-124-367A-20102	Sequence 20102, A	c 506	12	60.0	495	7	US-09-925-065A-625837	Sequence 625837,
c 434	12	60.0	201	17	US-11-124-367A-32739	Sequence 32739, A	c 507	12	60.0	495	7	US-09-925-065A-731731	Sequence 731731,
c 435	12	60.0	201	17	US-11-124-367A-32740	Sequence 32740, A	c 508	12	60.0	497	7	US-09-925-065A-314968	Sequence 314968,
c 436	12	60.0	351	7	US-09-925-065A-596207	Sequence 596207, A	c 509	12	60.0	499	7	US-09-925-065A-314969	Sequence 314969,
c 437	12	60.0	357	7	US-09-925-065A-16043	Sequence 16043, A	c 510	12	60.0	499	11	US-10-301-480-71481	Sequence 71481, A
c 438	12	60.0	357	11	US-10-301-480-117280	Sequence 117280, A	c 511	12	60.0	499	11	US-10-301-480-71482	Sequence 71482, A
c 439	12	60.0	357	12	US-10-301-480-730689	Sequence 730689, A	c 512	12	60.0	499	12	US-10-301-480-684890	Sequence 684890,
c 440	12	60.0	363	11	US-10-932-182A-5522	Sequence 5522, Ap	c 513	12	60.0	499	12	US-10-301-480-684891	Sequence 684891,
c 441	12	60.0	363	11	US-10-932-182A-5522	Sequence 5522, Ap	c 514	12	60.0	500	12	US-10-301-480-450237	Sequence 450237,
c 442	12	60.0	368	11	US-10-301-480-11386	Sequence 11386, A	c 515	12	60.0	500	12	US-10-301-480-450238	Sequence 450238,
c 443	12	60.0	408	12	US-10-301-480-624795	Sequence 624795, A	c 516	12	60.0	500	12	US-10-301-480-1063646	Sequence 1063646,
c 444	12	60.0	422	7	US-09-925-065A-55287	Sequence 55287, A	c 517	12	60.0	500	12	US-10-301-480-1063647	Sequence 1063647,
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c 448	12	60.0	437	7	US-09-925-065A-315234	Sequence 315234, A	c 521	12	60.0	505	7	US-09-925-065A-548845	Sequence 548845,
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C 529	12	60.0	510	7	US-09-925-065A-257180	Sequence 257180,	C 602	12	60.0	527	7	US-09-925-065A-20317	Sequence 20317, A
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C 548	12	60.0	516	12	US-10-301-480-949274	Sequence 949274,	C 621	12	60.0	532	12	US-10-301-480-735022	Sequence 735022,
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c 684	12	60.0	550	12	US-10-301-480-366942	Sequence 366942,	757	12	60.0	563	12	US-10-301-480-1106322	Sequence 1106322,
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c 696	12	60.0	551	12	US-10-301-480-1016556	Sequence 1016556,	c 769	12	60.0	565	12	US-10-301-480-327291	Sequence 327291,
c 697	12	60.0	551	12	US-10-301-480-1016557	Sequence 1016557,	c 770	12	60.0	565	12	US-10-301-480-822403	Sequence 822403,
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c 701	12	60.0	552	7	US-09-925-065A-588233	Sequence 588233, A	c 774	12	60.0	566	11	US-10-301-480-147481	Sequence 147481, A
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c 703	12	60.0	552	7	US-09-925-065A-605092	Sequence 605092, A	c 776	12	60.0	567	7	US-09-925-065A-805321	Sequence 805321,
c 704	12	60.0	552	11	US-10-301-480-127867	Sequence 127867,	c 777	12	60.0	567	7	US-09-925-065A-805322	Sequence 805322,
c 705	12	60.0	552	11	US-10-301-480-127868	Sequence 127868,	c 778	12	60.0	567	11	US-10-301-480-61533	Sequence 61533, A
c 706	12	60.0	552	11	US-10-301-480-127869	Sequence 127869,	c 779	12	60.0	568	12	US-10-301-480-674942	Sequence 674942,
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c 979      12 60.0 597 7 US-09-925-065A-805324 Sequence 805324,
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## ALIGNMENTS

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RESULT 1
US-11-136-527-226522/c
; Sequence 226522, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 226522
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-226522
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Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 21 GCCTTGGTTGGCAACACAT 2
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US-10-920-152-12/c
; Sequence 12, Application US/10920152
; Publication No. US20060057584A1
; GENERAL INFORMATION:
; APPLICANT: Baban, Soheyl
; APPLICANT: Bernard, Monique
; APPLICANT: Cherry, Elana
; APPLICANT: Gosselin, Diane
; APPLICANT: Hugo, Patrice
; APPLICANT: Malette, Brigitte
; APPLICANT: Miron, Pierre
; APPLICANT: Prive, Charles
; APPLICANT: Shazand, Kamran
; TITLE OF INVENTION: ENDOMETRIOSIS-RELATED MARKERS AND USES THEREOF
; FILE REFERENCE: 5600.71
; CURRENT APPLICATION NUMBER: US/10/920,152
; CURRENT FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: US/09/794,928
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/225,745
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: US 60/185,063
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-920-152-12
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 90 GCCTTGGTTGGCAACACAT 71
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US-11-136-527-4790/c
; Sequence 4790, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4790
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4790
Query Match 100.0%; Score 20; DB 17; Length 600;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 428 GCCTTGGTTGGCAACACAT 409
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RESULT 4



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US-11-136-527-694/c
; Sequence 694, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 694
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-694

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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAACACAT 20
Db 1631 GCTTTGGTTGGGCAACACAT 1612

RESULT 5
US-10-469-469-192/c
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; Publication No. US20060079493A1
; GENERAL INFORMATION:
; APPLICANT: FRITZ, LAWRENCE C.
; APPLICANT: BURROWS, FRANCIS J.
; TITLE OF INVENTION: METHODS FOR TREATING GENETICALLY-DEFINED PROLIFERATIVE
; TITLE OF INVENTION: DISORDERS WITH HSP90 INHIBITORS
; FILE REFERENCE: CON-0010-USN
; CURRENT APPLICATION NUMBER: US/10/469,469
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: PCT/US02/06518
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/272,751
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 192
; LENGTH: 3517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-469-469-192

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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAACACAT 20
Db 2022 GCTTTGGTTGGGCAACACAT 2003

RESULT 6
US-11-136-527-34022/c
; Sequence 34022, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25

US-11-136-527-694/c
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34022
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: Probe
US-11-136-527-34022

Query Match      95.0%; Score 19; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 CTTTGGTTGGGCAACACAT 7

RESULT 7
US-11-136-527-226492/c
; Sequence 226492, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 226492
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: Probe
US-11-136-527-226492

Query Match      95.0%; Score 19; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGGCAACACAT 20
Db 25 CTTTGGTTGGGCAACACAT 7

RESULT 8
US-11-136-527-226494/c
; Sequence 226494, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 226494
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURES:
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; OTHER INFORMATION: Probe  
US-11-136-527-226494

Query Match 95.0%; Score 19; DB 17; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.57;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACA 19  
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Db 19 GCTTTGGTTGGCAACACA 1

## RESULT 9

US-11-136-527-34046/c  
; Sequence 34046, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34046  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-34046

Query Match 90.0%; Score 18; DB 17; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTGTTGGGCAACACAT 20  
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Db 25 TTTGTTGGGCAACACAT 8

## RESULT 10

US-11-136-527-34023/c  
; Sequence 34023, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34023  
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; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-34023

Query Match 85.0%; Score 17; DB 17; Length 25;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTTGTTGGGCAACACAT 20  
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Db 25 TTGTTGGGCAACACAT 9

## RESULT 11

US-11-136-527-34042/c  
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; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34042  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-34042

Query Match 80.0%; Score 16; DB 17; Length 25;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGGTTGGGCAACACAT 20  
|||||  
Db 25 TGGTTGGGCAACACAT 10

## RESULT 12

US-10-301-480-546810  
; Sequence 546810, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 546810  
; LENGTH: 995  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-546810

Query Match 80.0%; Score 16; DB 12; Length 995;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGTTGGGCAACACA 19  
|||||  
Db 823 TTGTTGGGCAACACA 838

## RESULT 13

US-10-301-480-1160219  
; Sequence 1160219, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.

```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1160219
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1160219

Query Match      80.0%; Score 16; DB 12; Length 996;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TTGGTTGGGCACACA 19
Db      823 TTGGTTGGGCACACA 838
|||||

RESULT 14
US-10-301-480-553142/c
; Sequence 553142, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 553142
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-553142

Query Match      80.0%; Score 16; DB 12; Length 996;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTTGGTTGGGCAAC 16
Db      40 GCTTTGGTTGGGCAAC 25
|||||

RESULT 15
US-10-301-480-553488/c
; Sequence 553488, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1160219
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1160219

Query Match      80.0%; Score 16; DB 12; Length 996;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTTGGTTGGGCAAC 16
Db      40 GCTTTGGTTGGGCAAC 25
|||||

RESULT 16
US-10-301-480-1166551/c
; Sequence 1166551, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1166551
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1166551

Query Match      80.0%; Score 16; DB 12; Length 996;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTTGGTTGGGCAAC 16
Db      40 GCTTTGGTTGGGCAAC 25
|||||

RESULT 17
US-10-301-480-1166897/c
; Sequence 1166897, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1166897
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1166897

Query Match      80.0%; Score 16; DB 12; Length 996;
```

```
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 553488
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-553488

Query Match      80.0%; Score 16; DB 12; Length 996;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTTGGTTGGGCAAC 16
Db      40 GCTTTGGTTGGGCAAC 25
|||||

RESULT 16
US-10-301-480-1166551/c
; Sequence 1166551, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1166551
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1166551

Query Match      80.0%; Score 16; DB 12; Length 996;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTTGGTTGGGCAAC 16
Db      40 GCTTTGGTTGGGCAAC 25
|||||

RESULT 17
US-10-301-480-1166897/c
; Sequence 1166897, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1166897
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1166897

Query Match      80.0%; Score 16; DB 12; Length 996;
```

```
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAAC 16
Db 40 GCTTTGGTTGGGCAAC 25

RESULT 18
US-11-136-527-34024/c
; Sequence 34024, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34024
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-34024

Query Match 75.0%; Score 15; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTGGGCAACACAT 20
Db 25 GGTGGGCAACACAT 11

RESULT 19
US-10-301-480-541667
; Sequence 541667, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541667
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-541667

Query Match 75.0%; Score 15; DB 12; Length 1000;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAAC 15
Db 691 GCTTTGGTTGGGCAAC 705

RESULT 20
US-10-301-480-541667
; Sequence 541667, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541667
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-541667

Query Match 75.0%; Score 15; DB 12; Length 1000;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAAC 15
Db 691 GCTTTGGTTGGGCAAC 705

RESULT 21
US-09-925-065A-669805
; Sequence 669805, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 669805
; LENGTH: 1153
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-669805

Query Match 75.0%; Score 15; DB 7; Length 1153;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGGCAAC 16
Db 119 CTTTGGTTGGGCAAC 133

RESULT 22
US-10-115-609-22
; Sequence 22, Application US/10115609
; Publication No. US20060034826A1
```

```
US-10-301-480-1155076
; Sequence 1155076, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1155076
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-1155076

Query Match 75.0%; Score 15; DB 12; Length 1000;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAAC 15
Db 691 GCTTTGGTTGGGCAAC 705

RESULT 21
US-09-925-065A-669805
; Sequence 669805, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 669805
; LENGTH: 1153
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-669805

Query Match 75.0%; Score 15; DB 7; Length 1153;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGGCAAC 16
Db 119 CTTTGGTTGGGCAAC 133

RESULT 22
US-10-115-609-22
; Sequence 22, Application US/10115609
; Publication No. US20060034826A1
```

```

; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25760
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-25760

Query Match      70.0%; Score 14; DB 17; Length 201;
Best Local Similarity 100.0%; Pred.No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTTTGGTTGGGCA 14
        |||||
Db      67 GCTTTGGTTGGGCA 54

RESULT 25
US-09-925-065A-153801/c
; Sequence 153801, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153801
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-153801

Query Match      70.0%; Score 14; DB 7; Length 403;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CTTTGGTTGGGCAA 15
        |||||
Db      259 CTTTGGTTGGGCAA 246

RESULT 26
US-10-301-480-247396/c
; Sequence 247396, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21

```

; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 247396  
; LENGTH: 404  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-247396

Query Match 70.0%; Score 14; DB 12; Length 404;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGCAA 15  
|||  
Db 260 CTTTGGTTGGCAA 247

## RESULT 27

US-10-301-480-860805/c  
; Sequence 860805, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 860805  
; LENGTH: 404  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-860805

Query Match 70.0%; Score 14; DB 12; Length 404;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGCAA 15  
|||  
Db 260 CTTTGGTTGGCAA 247

## RESULT 28

US-10-301-480-14320/c  
; Sequence 14320, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14320  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-603534

; ORGANISM: Homo sapien  
US-10-301-480-14320

Query Match 70.0%; Score 14; DB 11; Length 468;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGGTTGGCAACA 17  
|||  
Db 185 TTGGTTGGCAACA 172

## RESULT 29

US-10-301-480-627729/c  
; Sequence 627729, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 627729  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-627729

Query Match 70.0%; Score 14; DB 12; Length 468;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGGTTGGCAACA 17  
|||  
Db 185 TTGGTTGGCAACA 172

## RESULT 30

US-09-925-065A-603534/c  
; Sequence 603534, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 603534  
; LENGTH: 506  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-603534

```
Query Match          70.0%; Score 14; DB 7; Length 506;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTTGGTTGGCAA 15
DB 21 CTTTGGTTGGCAA 8

RESULT 31
US-09-925-065A-603533/c
; Sequence 603533, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 603533
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-603533

Query Match          70.0%; Score 14; DB 7; Length 515;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTTGGTTGGCAA 15
DB 18 CTTTGGTTGGCAA 5

RESULT 32
US-10-301-480-425083
; Sequence 425083, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425083
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-425083

Query Match          70.0%; Score 14; DB 12; Length 535;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GCTTTGGTTGGCA 14
DB 336 GCTTTGGTTGGCA 349

RESULT 33
US-10-301-480-425084
; Sequence 425084, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425084
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-425084

Query Match          70.0%; Score 14; DB 12; Length 535;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCA 14
DB 336 GCTTTGGTTGGCA 349

RESULT 34
US-10-301-480-425085
; Sequence 425085, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425085
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-425085

Query Match          70.0%; Score 14; DB 12; Length 535;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCA 14
DB 336 GCTTTGGTTGGCA 349

RESULT 35
US-10-301-480-1038492
; Sequence 1038492, Application US/10301480
```



```
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1038492
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1038492

Query Match          70.0%; Score 14; DB 12; Length 535;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCA 14
   |||||
Db 336 GCTTTGGTTGGGCA 349

RESULT 36
US-10-301-480-1038493
; Sequence 1038493, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1038493
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1038493

Query Match          70.0%; Score 14; DB 12; Length 535;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCA 14
   |||||
Db 336 GCTTTGGTTGGGCA 349

RESULT 37
US-10-301-480-1038494
; Sequence 1038494, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1038492
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1038492
```

```
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1038494
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1038494

Query Match          70.0%; Score 14; DB 12; Length 535;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCA 14
   |||||
Db 336 GCTTTGGTTGGGCA 349

RESULT 38
US-09-925-065A-353424
; Sequence 353424, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 353424
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-353424

Query Match          70.0%; Score 14; DB 7; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCA 14
   |||||
Db 336 GCTTTGGTTGGGCA 349

RESULT 39
US-09-925-065A-353425
; Sequence 353425, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
```

```
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 353425
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-353425
```

```
Query Match 70.0%; Score 14; DB 7; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GCTTTGGTTGGGCA 14
|||||
DB 336 GCTTTGGTTGGGCA 349
```

## RESULT 40

```
US-09-925-065A-353426
; Sequence 353426, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 353426
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-353426
```

```
Query Match 70.0%; Score 14; DB 7; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GCTTTGGTTGGGCA 14
|||||
DB 336 GCTTTGGTTGGGCA 349
```

## RESULT 41

```
US-09-925-065A-603532/c
; Sequence 603532, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
```

```
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 603532
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-603532
```

```
Query Match 70.0%; Score 14; DB 7; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 CTTTGGTTGGGCAA 15
|||||
DB 368 CTTTGGTTGGGCAA 355
```

## RESULT 42

```
US-09-925-065A-94527/c
; Sequence 94527, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94527
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-94527
```

```
Query Match 70.0%; Score 14; DB 7; Length 545;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 GGTGGGCAACACA 19
|||||
DB 109 GGTGGGCAACACA 96
```

## RESULT 43

```
US-10-301-480-195769/c
; Sequence 195769, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
```

```
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 195769
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-195769
```

```
Query Match 70.0%; Score 14; DB 11; Length 545;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 GGTGGGCAACACA 19
Db 109 GGTGGGCAACACA 96
|||||
```

## RESULT 44

```
US-10-301-480-809178/c
; Sequence 809178, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 809178
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-809178
```

```
Query Match 70.0%; Score 14; DB 12; Length 545;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 GGTGGGCAACACA 19
Db 109 GGTGGGCAACACA 96
|||||
```

## RESULT 45

```
US-10-301-480-415497/c
; Sequence 415497, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 415497
```

```
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-415497
```

```
Query Match 70.0%; Score 14; DB 12; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 GGTGGGCAACACA 19
Db 293 GGTGGGCAACACA 280
|||||
```

## RESULT 46

```
US-10-301-480-415498/c
; Sequence 415498, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 415498
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-415498
```

```
Query Match 70.0%; Score 14; DB 12; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 GGTGGGCAACACA 19
Db 293 GGTGGGCAACACA 280
|||||
```

## RESULT 47

```
US-10-301-480-1028906/c
; Sequence 1028906, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1028906
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1028906
```

```
Query Match 70.0%; Score 14; DB 12; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 6 GGTGGGCAACACA 19  
Db 293 GGTGGGCAACACA 280

## RESULT 48

US-10-301-480-1028907/c  
; Sequence 1028907, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1028907  
; LENGTH: 556  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-1028907

Query Match 70.0%; Score 14; DB 12; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGTGGGCAACACA 19  
Db 293 GGTGGGCAACACA 280

## RESULT 49

US-09-925-065A-386479  
; Sequence 386479, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 386479  
; LENGTH: 562  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-386479

Query Match 70.0%; Score 14; DB 7; Length 562;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGTTGGCAACA 17  
Db 58 TTGGTTGGCAACA 71

## RESULT 50

US-10-301-480-455055  
; Sequence 455055, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 455055  
; LENGTH: 564  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-455055

Query Match 70.0%; Score 14; DB 12; Length 564;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGTTGGCAACA 17  
Db 58 TTGGTTGGCAACA 71

Search completed: May 8, 2006, 01:26:57  
Job time : 447 secs

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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 22:42:33 ; Search time 1045 Seconds  
(without alignments)  
158.266 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20

Sequence: 1 gcttggtgggaacacat 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	7	US-10-671-074-172
2	20	100.0	25	8	US-10-719-900-85415
3	20	100.0	254	3	US-09-794-928A-12
4	20	100.0	303	7	US-10-242-535A-24143
5	20	100.0	303	7	US-10-085-783A-24143
6	20	100.0	447	7	US-10-242-535A-35649
7	20	100.0	447	7	US-10-085-783A-35649
8	20	100.0	520	9	US-10-505-680-708
9	20	100.0	2514	9	US-10-450-763-20856
10	20	100.0	2827	7	US-10-391-530-1
11	20	100.0	3200	7	US-10-391-530-3
12	20	100.0	3517	7	US-10-391-530-2
13	20	100.0	4945	7	US-10-671-074-11
14	20	100.0	5723	6	US-10-007-926A-134
15	20	100.0	5723	6	US-10-341-434-52
16	20	100.0	5723	7	US-10-671-074-4
17	20	100.0	5723	9	US-10-956-157-760
18	20	100.0	5833	9	US-10-450-763-20857
19	19	95.0	20	7	US-10-671-074-40
20	19	95.0	20	7	US-10-671-074-118
21	17	85.0	2000	3	US-09-938-842A-4239
22	17	85.0	2000	3	US-09-938-842A-4239
23	16	80.0	20	7	US-10-671-074-41

C	24	16	80.0	20	7	US-10-671-074-119	Sequence 119, App
		16	80.0	4106	3	US-09-764-891-7739	Sequence 7739, Ap
c	26	15	75.0	25	7	US-10-719-956-641503	Sequence 641503,
c	27	15	75.0	25	8	US-10-719-900-643422	Sequence 643422,
c	28	15	75.0	405	7	US-10-424-599-107214	Sequence 107214,
c	29	15	75.0	406	7	US-10-430-201-4459	Sequence 4459, Ap
c	30	15	75.0	406	7	US-10-430-201-4460	Sequence 4460, Ap
c	31	15	75.0	498	3	US-09-918-995-32485	Sequence 32485, A
c	32	15	75.0	574	3	US-09-764-872-161	Sequence 161, App
c	33	15	75.0	602	8	US-10-425-115-78789	Sequence 78789, A
c	34	15	75.0	1153	4	US-09-925-065A-669805	Sequence 669805,
c	35	15	75.0	1263	9	US-10-450-763-11672	Sequence 11672, A
c	36	15	75.0	1342	3	US-09-956-004-66	Sequence 66, Appl
c	37	15	75.0	1342	8	US-10-808-570-66	Sequence 66, Appl
c	38	15	75.0	1550	6	US-10-108-260A-1546	Sequence 1546, Ap
c	39	15	75.0	2154	7	US-10-282-122A-9084	Sequence 9084, Ap
c	40	15	75.0	3059	6	US-10-094-749-916	Sequence 916, App
c	41	15	75.0	3342	10	US-11-097-143-32554	Sequence 32554, A
c	42	15	75.0	3366	10	US-11-097-143-23078	Sequence 23078, A
c	43	15	75.0	3593	5	US-10-002-775-10	Sequence 10, Appl
c	44	15	75.0	3593	5	US-10-115-615-22	Sequence 22, Appl
c	45	15	75.0	3593	9	US-10-764-420-1546	Sequence 1546, Ap
c	46	15	75.0	3593	9	US-10-631-467-1140	Sequence 1140, Ap
c	47	15	75.0	5205	8	US-10-758-672A-18	Sequence 18, Appl
c	48	15	75.0	5205	9	US-10-758-636A-18	Sequence 18, Appl
c	49	15	75.0	5466	8	US-10-357-819-9	Sequence 9, Appl
c	50	15	75.0	5492	10	US-11-097-143-23077	Sequence 23077, A
c	51	15	75.0	6308	8	US-10-758-672A-1	Sequence 1, Appl
c	52	15	75.0	6308	9	US-10-758-636A-1	Sequence 1, Appl
c	53	15	75.0	7742	6	US-10-287-218-22	Sequence 22, Appl
c	54	15	75.0	7742	7	US-10-474-291-22	Sequence 22, Appl
c	55	15	908766	9	US-10-795-159-685	Sequence 685, App	
c	56	15	75.0	1830121	7	US-10-329-670-1	Sequence 1, Appl
c	57	15	75.0	1830121	8	US-10-158-865-1	Sequence 1, Appl
c	58	15	75.0	1830121	9	US-10-981-687-1	Sequence 1, Appl
c	59	14	70.0	20	7	US-10-688-706-95	Sequence 95, Appl
c	60	14	70.0	20	7	US-10-688-706-125	Sequence 125, App
c	61	14	70.0	20	7	US-10-688-706-141	Sequence 141, App
c	62	14	70.0	20	7	US-10-688-706-170	Sequence 170, App
c	63	14	70.0	20	7	US-10-688-706-273	Sequence 273, App
c	64	14	70.0	20	7	US-10-688-706-695	Sequence 695, App
c	65	14	70.0	20	7	US-10-688-706-727	Sequence 727, App
c	66	14	70.0	25	8	US-10-719-900-219203	Sequence 219203,
c	67	14	70.0	229	3	US-09-922-293-1203	Sequence 1203, Ap
c	68	14	70.0	231	3	US-09-922-293-1201	Sequence 1201, Ap
c	69	14	70.0	266	3	US-09-922-293-1220	Sequence 1220, Ap
c	70	14	70.0	296	6	US-10-029-386-23544	Sequence 23544, A
c	71	14	70.0	306	10	US-11-097-143-29267	Sequence 29267, A
c	72	14	70.0	317	7	US-10-424-599-126752	Sequence 126752,
c	73	14	70.0	387	7	US-10-242-535A-33973	Sequence 33973, A
c	74	14	70.0	387	7	US-10-085-783A-33973	Sequence 33973, A
c	75	14	70.0	403	4	US-09-925-065A-153801	Sequence 153801,
c	76	14	70.0	404	3	US-09-922-293-1224	Sequence 1224, Ap
c	77	14	70.0	419	3	US-09-922-293-1230	Sequence 1230, Ap
c	78	14	70.0	426	3	US-09-783-590-10461	Sequence 10461, A
c	79	14	70.0	440	3	US-09-866-050A-77	Sequence 77, Appl
c	80	14	70.0	440	5	US-10-152-661-77	Sequence 77, Appl
c	81	14	70.0	471	3	US-09-918-995-31180	Sequence 31180, A
c	82	14	70.0	493	5	US-10-027-632-78715	Sequence 78715, A
c	83	14	70.0	493	5	US-10-027-632-78716	Sequence 78716, A
c	84	14	70.0	493	6	US-10-027-632-78715	Sequence 78715, A
c	85	14	70.0	493	6	US-10-027-632-78716	Sequence 78716, A
c	86	14	70.0	501	9	US-10-972-079-75011	Sequence 75011, A
c	87	14	70.0	504	6	US-10-029-386-9844	Sequence 9844, Ap
c	88	14	70.0	506	4	US-09-925-065A-603534	Sequence 603534,
c	89	14	70.0	515	4	US-09-925-065A-603533	Sequence 603533,
c	90	14	70.0	517	5	US-10-027-632-113357	Sequence 113357,
c	91	14	70.0	517	6	US-10-027-632-113357	Sequence 113357,
c	92	14	70.0	537	4	US-09-925-065A-353424	Sequence 353424,
c	93	14	70.0	537	4	US-09-925-065A-353425	Sequence 353425,
c	94	14	70.0	537	4	US-09-925-065A-353426	Sequence 353426,
c	95	14	70.0	538	4	US-09-925-065A-603532	Sequence 603532,
c	96	14	70.0	545	4	US-09-925-065A-94527	Sequence 94527, A

c 97	14	70.0	562	4	US-09-925-065A-386479	Sequence 386479,	c 170	14	70.0	2197	9	US-10-956-157-1519	Sequence 1519, Ap
c 98	14	70.0	567	4	US-09-925-065A-342764	Sequence 342764,	c 171	14	70.0	2197	7	US-10-756-149-169	Sequence 169, App
c 99	14	70.0	567	4	US-09-925-065A-342765	Sequence 342765,	c 172	14	70.0	2218	7	US-10-424-599-59900	Sequence 59900, A
c 100	14	70.0	587	4	US-09-925-065A-605689	Sequence 605689,	c 173	14	70.0	2227	8	US-10-723-860-7344	Sequence 7344, Ap
c 101	14	70.0	592	4	US-09-925-065A-199507	Sequence 199507,	c 174	14	70.0	2306	10	US-11-097-143-29266	Sequence 29266, A
c 102	14	70.0	592	4	US-09-925-065A-463575	Sequence 463575,	c 175	14	70.0	2314	5	US-10-027-632-261567	Sequence 261567,
c 103	14	70.0	592	4	US-09-925-065A-463576	Sequence 463576,	c 176	14	70.0	2314	5	US-10-027-632-261568	Sequence 261568,
c 104	14	70.0	592	4	US-09-925-065A-463577	Sequence 463577,	c 177	14	70.0	2314	6	US-10-027-632-261567	Sequence 261567,
c 105	14	70.0	592	4	US-09-925-065A-463578	Sequence 463578,	c 178	14	70.0	2314	6	US-10-027-632-261568	Sequence 261568,
c 106	14	70.0	593	7	US-10-021-323-14958	Sequence 14958, A	c 179	14	70.0	2393	7	US-10-236-115-577	Sequence 577, App
c 107	14	70.0	601	4	US-09-925-065A-540729	Sequence 540729,	c 180	14	70.0	2407	8	US-10-357-930-21308	Sequence 21308, A
c 108	14	70.0	602	4	US-09-925-065A-902618	Sequence 902618,	c 181	14	70.0	2407	8	US-10-357-930-23642	Sequence 23642, A
c 109	14	70.0	606	4	US-09-925-065A-199508	Sequence 199508,	c 182	14	70.0	2407	8	US-10-357-930-27150	Sequence 27150, A
c 110	14	70.0	611	4	US-09-925-065A-487106	Sequence 487106,	c 183	14	70.0	2407	8	US-10-357-930-29533	Sequence 29533, A
c 111	14	70.0	631	5	US-10-027-632-145308	Sequence 145308,	c 184	14	70.0	2407	8	US-10-450-763-23736	Sequence 23736, A
c 112	14	70.0	631	6	US-10-027-632-145308	Sequence 145308,	c 185	14	70.0	2439	7	US-10-052-482-228	Sequence 228, App
c 113	14	70.0	632	8	US-10-357-930-57240	Sequence 57240, A	c 186	14	70.0	2586	5	US-10-084-817-173	Sequence 173, App
c 114	14	70.0	646	5	US-10-027-632-68455	Sequence 68455, A	c 187	14	70.0	2793	9	US-10-486-970-1	Sequence 1, Appli
c 115	14	70.0	646	6	US-10-027-632-68455	Sequence 68455, A	c 188	14	70.0	2935	7	US-10-052-482-227	Sequence 227, App
c 116	14	70.0	661	4	US-09-925-065A-884132	Sequence 884132,	c 189	14	70.0	3036	6	US-10-369-493-26431	Sequence 26431, A
c 117	14	70.0	707	3	US-09-902-563-7	Sequence 7, Appli	c 190	14	70.0	3082	6	US-10-354-358-33	Sequence 33, Appl
c 118	14	70.0	707	5	US-10-096-255-7	Sequence 7, Appli	c 191	14	70.0	3082	7	US-10-688-706-3070	Sequence 3070, Ap
c 119	14	70.0	707	9	US-10-997-920-7	Sequence 7, Appli	c 192	14	70.0	3082	8	US-10-737-450-63	Sequence 63, Appl
c 120	14	70.0	723	9	US-10-504-328-5	Sequence 5, Appli	c 193	14	70.0	3082	8	US-10-753-267-11	Sequence 11, Appl
c 121	14	70.0	748	9	US-10-724-264A-30	Sequence 30, Appl	c 194	14	70.0	3082	9	US-10-831-704-68	Sequence 68, Appl
c 122	14	70.0	750	3	US-09-847-513A-8	Sequence 8, Appli	c 195	14	70.0	3082	9	US-10-956-157-767	Sequence 767, App
c 123	14	70.0	750	3	US-09-847-513A-14	Sequence 14, Appl	c 196	14	70.0	3082	9	US-10-756-149-1758	Sequence 1758, Ap
c 124	14	70.0	750	3	US-09-847-513A-26	Sequence 26, Appl	c 197	14	70.0	3136	7	US-10-262-511-121	Sequence 121, App
c 125	14	70.0	750	3	US-09-847-513A-28	Sequence 28, Appl	c 198	14	70.0	3256	4	US-09-925-065A-688254	Sequence 688254,
c 126	14	70.0	750	3	US-09-847-513A-36	Sequence 36, Appl	c 199	14	70.0	4169	10	US-11-097-143-40138	Sequence 40138, A
c 127	14	70.0	753	9	US-10-724-264A-10	Sequence 10, Appl	c 200	14	70.0	4963	9	US-10-450-763-14200	Sequence 14200, A
c 128	14	70.0	753	9	US-10-724-264A-19	Sequence 19, Appl	c 201	14	70.0	5030	10	US-11-097-143-19477	Sequence 19477, A
c 129	14	70.0	753	9	US-10-724-264A-20	Sequence 20, Appl	c 202	14	70.0	5358	10	US-11-097-143-13135	Sequence 13135, A
c 130	14	70.0	753	9	US-10-724-264A-22	Sequence 22, Appl	c 203	14	70.0	5403	3	US-09-902-563-3	Sequence 3, Appli
c 131	14	70.0	774	7	US-10-424-599-119148	Sequence 119148,	c 204	14	70.0	5403	5	US-10-096-255-3	Sequence 3, Appli
c 132	14	70.0	787	7	US-10-437-963-95032	Sequence 95032, A	c 205	14	70.0	5403	3	US-10-997-920-3	Sequence 3, Appli
c 133	14	70.0	816	6	US-10-369-493-27565	Sequence 27565, A	c 206	14	70.0	5502	3	US-09-349-058-45	Sequence 45, Appl
c 134	14	70.0	825	9	US-10-504-328-3	Sequence 3, Appli	c 207	14	70.0	5502	5	US-10-040-430-45	Sequence 45, Appl
c 135	14	70.0	887	3	US-09-764-877-2110	Sequence 2110, Ap	c 208	14	70.0	5555	5	US-10-450-763-29829	Sequence 29829, A
c 136	14	70.0	887	3	US-09-764-877-2112	Sequence 2112, Ap	c 209	14	70.0	8002	10	US-11-097-143-13348	Sequence 13348, A
c 137	14	70.0	887	6	US-10-242-515-2110	Sequence 2110, Ap	c 210	14	70.0	10271	3	US-09-754-468-43	Sequence 43, Appl
c 138	14	70.0	887	6	US-10-242-515-2112	Sequence 2112, Ap	c 211	14	70.0	14283	10	US-11-097-143-14938	Sequence 14938, A
c 139	14	70.0	921	3	US-09-764-877-2111	Sequence 2111, Ap	c 212	14	70.0	16995	7	US-08-961-527-82	Sequence 82, Appl
c 140	14	70.0	921	6	US-10-242-515-2111	Sequence 2111, Ap	c 213	14	70.0	16995	7	US-10-158-844-82	Sequence 82, Appl
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c 144	14	70.0	1155	7	US-10-437-963-49492	Sequence 49492, A	c 217	14	70.0	50927	7	US-10-367-094-56	Sequence 56, Appl
c 145	14	70.0	1157	9	US-10-450-763-25810	Sequence 25810, A	c 218	14	70.0	52192	8	US-10-741-600-17615	Sequence 17615, A
c 146	14	70.0	1194	9	US-10-617-320-294	Sequence 294, Appl	c 219	14	70.0	89328	3	US-09-873-367C-332	Sequence 332, App
c 147	14	70.0	1279	3	US-09-765-272-47	Sequence 47, Appl	c 220	14	70.0	89328	9	US-10-843-641A-332	Sequence 332, App
c 148	14	70.0	1279	10	US-11-106-649-47	Sequence 47, Appl	c 221	14	70.0	96597	7	US-10-052-482-226	Sequence 226, App
c 149	14	70.0	1281	8	US-10-472-928-639	Sequence 639, App	c 222	14	70.0	104729	9	US-10-723-860-1434	Sequence 1434, Ap
c 150	14	70.0	1301	8	US-10-425-115-140395	Sequence 140395,	c 223	14	70.0	104729	8	US-10-756-149-1398	Sequence 1398, Ap
c 151	14	70.0	1308	9	US-10-617-320-1653	Sequence 1653, Ap	c 224	14	70.0	137908	9	US-10-287-436A-779	Sequence 779, App
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c 153	14	70.0	1400	9	US-10-956-157-6754	Sequence 6754, Ap	c 226	14	70.0	201239	8	US-10-278-698-760	Sequence 760, App
c 154	14	70.0	1448	9	US-10-287-436A-952	Sequence 952, App	c 227	14	70.0	2162598	8	US-10-472-928-4979	Sequence 4979, Ap
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c 157	14	70.0	1588	7	US-10-282-122A-12182	Sequence 12182, A	c 230	13	65.0	20	7	US-10-688-706-1058	Sequence 1058, Ap
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c 166	14	70.0	2179	7	US-10-437-963-49495	Sequence 49495, A	c 239	13	65.0	25	10	US-11-036-317-555889	Sequence 555889,
c 167	14	70.0	2196	4	US-09-925-065A-683172	Sequence 683172,	c 240	13	65.0	25	10	US-11-036-317-721238	Sequence 721238,
c 168	14	70.0	2197	6	US-10-172-118-1228	Sequence 1228, Ap	c 241	13	65.0	60	3	US-09-908-975-11722	Sequence 11722, A
c 169	14	70.0	2197	7	US-10-342-887-1228	Sequence 1228, Ap	c 242	13	65.0	143	3	US-09-815-242-2038	Sequence 2038, Ap



C 243	13	65.0	143	7	US-10-282-122A-4568	Sequence 4568, Ap	C 316	13	65.0	566	7	US-10-767-701-1060	Sequence 1060, Ap
C 244	13	65.0	161	3	US-09-983-648A-4	Sequence 4, Appli	C 317	13	65.0	567	3	US-09-796-632-4178	Sequence 4178, Ap
C 245	13	65.0	168	3	US-09-747-377-54	Sequence 54, Appli	C 318	13	65.0	567	5	US-10-040-862-4178	Sequence 4178, Ap
C 246	13	65.0	168	5	US-10-105-613-54	Sequence 54, Appli	C 319	13	65.0	567	6	US-10-057-475B-4178	Sequence 4178, Ap
C 247	13	65.0	201	7	US-10-741-601-25881	Sequence 25881, A	C 320	13	65.0	567	6	US-10-154-884B-4178	Sequence 4178, Ap
C 248	13	65.0	201	7	US-10-741-601-25909	Sequence 25909, A	C 321	13	65.0	567	8	US-10-764-324-4178	Sequence 4178, Ap
C 249	13	65.0	201	8	US-10-719-993-34294	Sequence 34294, A	C 322	13	65.0	572	5	US-10-027-632-209217	Sequence 209217, Ap
C 250	13	65.0	216	6	US-10-339-740-208	Sequence 208, App	C 323	13	65.0	572	5	US-10-027-632-218643	Sequence 218643, Ap
C 251	13	65.0	231	7	US-10-437-963-21400	Sequence 21400, A	C 324	13	65.0	572	6	US-10-027-632-209217	Sequence 209217, Ap
C 252	13	65.0	258	7	US-10-424-598-1814	Sequence 1814, Ap	C 325	13	65.0	572	6	US-10-027-632-218643	Sequence 218643, Ap
C 253	13	65.0	277	7	US-10-767-701-11706	Sequence 11706, A	C 326	13	65.0	572	9	US-10-972-079-68767	Sequence 68767, A
C 254	13	65.0	277	7	US-10-424-599-14939	Sequence 14939, A	C 327	13	65.0	574	7	US-10-767-701-23865	Sequence 23865, A
C 255	13	65.0	281	7	US-10-424-599-715	Sequence 715, App	C 328	13	65.0	577	8	US-10-425-115-42360	Sequence 42360, A
C 256	13	65.0	289	3	US-09-867-701-7257	Sequence 7257, Ap	C 329	13	65.0	579	7	US-10-437-963-6891	Sequence 6891, Ap
C 257	13	65.0	300	9	US-10-779-543-6238	Sequence 6238, Ap	C 330	13	65.0	580	6	US-10-029-386-1698	Sequence 1698, Ap
C 258	13	65.0	322	7	US-10-424-599-9127	Sequence 9127, Ap	C 331	13	65.0	588	4	US-09-925-065A-521903	Sequence 521903, Ap
C 259	13	65.0	340	8	US-10-425-115-111286	Sequence 111286, A	C 332	13	65.0	590	4	US-09-925-065A-246451	Sequence 246451, Ap
C 260	13	65.0	350	7	US-10-424-599-5044	Sequence 5044, Ap	C 333	13	65.0	591	4	US-09-925-065A-648059	Sequence 648059, Ap
C 261	13	65.0	353	3	US-09-815-249-2139	Sequence 2139, Ap	C 334	13	65.0	591	4	US-09-925-065A-935924	Sequence 935924, Ap
C 262	13	65.0	353	7	US-10-282-122A-4704	Sequence 4704, Ap	C 335	13	65.0	591	4	US-09-925-065A-935925	Sequence 935925, Ap
C 263	13	65.0	377	3	US-09-864-408A-5619	Sequence 5619, Ap	C 336	13	65.0	592	4	US-09-925-065A-335272	Sequence 335272, Ap
C 264	13	65.0	377	4	US-09-925-065A-491370	Sequence 491370, A	C 337	13	65.0	595	9	US-10-972-079-86171	Sequence 86171, A
C 265	13	65.0	387	8	US-10-425-115-866	Sequence 866, App	C 338	13	65.0	596	4	US-09-925-065A-754854	Sequence 754854, Ap
C 266	13	65.0	394	8	US-10-425-115-103841	Sequence 103841, A	C 339	13	65.0	596	4	US-09-925-065A-754855	Sequence 754855, Ap
C 267	13	65.0	398	7	US-10-437-963-56425	Sequence 56425, A	C 340	13	65.0	596	4	US-09-925-065A-825513	Sequence 825513, Ap
C 268	13	65.0	400	2	US-08-781-986A-2971	Sequence 2971, Ap	C 341	13	65.0	598	5	US-10-027-632-248084	Sequence 248084, Ap
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C 270	13	65.0	401	8	US-10-425-115-108634	Sequence 108634, A	C 343	13	65.0	598	6	US-10-027-632-248085	Sequence 248085, Ap
C 271	13	65.0	404	7	US-10-424-599-49377	Sequence 49377, A	C 344	13	65.0	598	6	US-10-027-632-248085	Sequence 248085, Ap
C 272	13	65.0	407	8	US-10-425-115-56471	Sequence 56471, A	C 345	13	65.0	599	5	US-10-027-632-45269	Sequence 45269, A
C 273	13	65.0	410	7	US-10-424-599-15645	Sequence 15645, A	C 346	13	65.0	599	5	US-10-027-632-92411	Sequence 92411, A
C 274	13	65.0	416	7	US-10-424-599-100021	Sequence 100021, A	C 347	13	65.0	599	5	US-10-027-632-307601	Sequence 307601, A
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C 278	13	65.0	438	8	US-10-425-115-183222	Sequence 183222, A	C 351	13	65.0	600	9	US-10-972-079-26509	Sequence 26509, A
C 279	13	65.0	445	6	US-10-914-037-17	Sequence 17, Appli	C 352	13	65.0	600	9	US-10-972-079-26510	Sequence 26510, A
C 280	13	65.0	456	6	US-10-369-493-43615	Sequence 43615, A	C 353	13	65.0	600	9	US-10-972-079-26511	Sequence 26511, A
C 281	13	65.0	486	8	US-10-914-037-18	Sequence 18, Appli	C 354	13	65.0	600	9	US-10-972-079-26512	Sequence 26512, A
C 282	13	65.0	487	5	US-10-027-632-11192	Sequence 11192, A	C 355	13	65.0	600	9	US-10-972-079-28516	Sequence 28516, A
C 283	13	65.0	487	6	US-10-027-632-11192	Sequence 11192, A	C 356	13	65.0	600	9	US-10-972-079-43227	Sequence 43227, A
C 284	13	65.0	488	8	US-10-425-115-126141	Sequence 126141, A	C 357	13	65.0	600	9	US-10-972-079-43228	Sequence 43228, A
C 285	13	65.0	495	5	US-10-060-036-4296	Sequence 4296, Ap	C 358	13	65.0	600	9	US-10-972-079-44504	Sequence 44504, A
C 286	13	65.0	495	8	US-10-425-115-22728	Sequence 22728, A	C 359	13	65.0	600	9	US-10-972-079-88827	Sequence 88827, A
C 287	13	65.0	499	7	US-10-424-599-11028	Sequence 11028, A	C 360	13	65.0	600	9	US-10-972-079-96029	Sequence 96029, A
C 288	13	65.0	511	4	US-09-925-065A-60422	Sequence 60422, A	C 361	13	65.0	609	4	US-09-925-065A-478182	Sequence 478182, Ap
C 289	13	65.0	515	4	US-09-925-065A-590910	Sequence 590910, A	C 362	13	65.0	609	4	US-09-925-065A-478183	Sequence 478183, Ap
C 290	13	65.0	520	4	US-09-925-065A-545704	Sequence 545704, A	C 363	13	65.0	613	5	US-10-027-632-130886	Sequence 130886, Ap
C 291	13	65.0	520	4	US-09-925-065A-545705	Sequence 545705, A	C 364	13	65.0	613	5	US-10-027-632-130887	Sequence 130887, Ap
C 292	13	65.0	521	5	US-10-027-632-89361	Sequence 89361, A	C 365	13	65.0	613	5	US-10-027-632-130888	Sequence 130888, Ap
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C 294	13	65.0	521	6	US-10-027-632-89361	Sequence 89361, A	C 367	13	65.0	613	6	US-10-027-632-130887	Sequence 130887, Ap
C 295	13	65.0	521	6	US-10-027-632-89362	Sequence 89362, A	C 368	13	65.0	613	6	US-10-027-632-130888	Sequence 130888, Ap
C 296	13	65.0	526	6	US-10-029-386-844	Sequence 844, App	C 369	13	65.0	616	4	US-09-925-065A-471520	Sequence 471520, Ap
C 297	13	65.0	528	4	US-09-925-065A-224786	Sequence 224786, A	C 370	13	65.0	617	6	US-10-204-836-3	Sequence 3, Appli
C 298	13	65.0	529	3	US-09-920-300A-1580	Sequence 1580, Ap	C 371	13	65.0	621	4	US-09-925-065A-481726	Sequence 481726, Ap
C 299	13	65.0	529	5	US-10-033-528-1580	Sequence 1580, Ap	C 372	13	65.0	621	4	US-09-925-065A-481727	Sequence 481727, Ap
C 300	13	65.0	529	6	US-10-099-926-1580	Sequence 1580, Ap	C 373	13	65.0	623	7	US-10-437-963-6019	Sequence 6019, Ap
C 301	13	65.0	529	7	US-10-961-527-1580	Sequence 1580, Ap	C 374	13	65.0	625	5	US-10-027-632-302200	Sequence 302200, Ap
C 302	13	65.0	540	9	US-10-437-963-90426	Sequence 90426, A	C 375	13	65.0	625	5	US-10-027-632-302200	Sequence 302200, Ap
C 303	13	65.0	542	4	US-09-925-065A-755300	Sequence 755300, A	C 376	13	65.0	625	6	US-10-027-632-82523	Sequence 82523, A
C 304	13	65.0	545	4	US-09-925-065A-471519	Sequence 471519, A	C 377	13	65.0	631	6	US-10-027-632-302200	Sequence 302200, Ap
C 305	13	65.0	545	4	US-09-925-065A-471521	Sequence 471521, A	C 378	13	65.0	631	6	US-09-925-065A-411439	Sequence 411439, Ap
C 306	13	65.0	545	4	US-09-925-065A-471522	Sequence 471522, A	C 379	13	65.0	633	5	US-10-027-632-207358	Sequence 207358, Ap
C 307	13	65.0	546	4	US-09-925-065A-95641	Sequence 95641, A	C 380	13	65.0	633	6	US-10-027-632-207358	Sequence 207358, Ap
C 308	13	65.0	546	4	US-09-925-065A-95642	Sequence 95642, A	C 381	13	65.0	638	4	US-09-925-065A-49102	Sequence 49102, A
C 309	13	65.0	547	4	US-09-925-065A-507101	Sequence 507101, A	C 382	13	65.0	647	4	US-09-925-065A-512632	Sequence 512632, Ap
C 310	13	65.0	555	4	US-09-925-065A-333718	Sequence 333718, A	C 383	13	65.0	647	4	US-09-925-065A-512633	Sequence 512633, Ap
C 311	13	65.0	558	4	US-09-925-065A-640608	Sequence 640608, A	C 384	13	65.0	647	5	US-10-027-632-102334	Sequence 102334, Ap
C 312	13	65.0	558	7	US-10-282-132A-22137	Sequence 22137, A	C 385	13	65.0	647	6	US-10-027-632-102334	Sequence 102334, Ap
C 313	13	65.0	558	7	US-10-424-599-11211	Sequence 11211, A	C 386	13	65.0	655	3	US-09-864-408A-4283	Sequence 4283, Ap
C 314	13	65.0	559	4	US-09-925-065A-391767	Sequence 391767, A	C 387	13	65.0	655	4	US-09-925-065A-763741	Sequence 763741, Ap
C 315	13	65.0	559	5	US-10-060-036-1381	Sequence 1381, Ap	C 388	13	65.0	655	4	US-09-925-065A-763742	Sequence 763742, Ap

C 399	13	65.0	656	4	US-09-925-065A-771621, Sequence 771621,	Sequence 771621,	13	65.0	1161	2	US-08-781-986A-497	Sequence 497, App
C 390	13	65.0	656	4	US-09-925-065A-771622, Sequence 771622,	Sequence 771622,	13	65.0	1161	7	US-10-329-624-497	Sequence 497, App
C 391	13	65.0	658	4	US-09-925-065A-882868 Sequence 882868,	Sequence 882868,	13	65.0	1163	7	US-10-425-114-22074	Sequence 22074, A
C 392	13	65.0	658	4	US-09-925-065A-889432 Sequence 889432,	Sequence 889432,	13	65.0	1186	8	US-10-739-930-4848	Sequence 4848, Ap
C 393	13	65.0	666	8	US-10-425-115-10304 Sequence 10304, A	Sequence 10304, A	13	65.0	1193	7	US-10-437-963-10611	Sequence 10611, A
C 394	13	65.0	670	7	US-10-767-701-26141 Sequence 26141, A	Sequence 26141, A	13	65.0	1200	4	US-09-925-065A-2692	Sequence 2692, Ap
C 395	13	65.0	683	4	US-09-925-065A-79305 Sequence 79305, A	Sequence 79305, A	13	65.0	1206	4	US-09-925-065A-2693	Sequence 2693, Ap
C 396	13	65.0	692	5	US-10-027-632-99365 Sequence 99365, A	Sequence 99365, A	13	65.0	1220	4	US-10-398-221-1123	Sequence 1123, Ap
C 397	13	65.0	692	6	US-10-027-632-99366 Sequence 99366, A	Sequence 99366, A	13	65.0	1245	5	US-10-027-632-207357	Sequence 207357,
C 398	13	65.0	692	6	US-10-027-632-99366 Sequence 99366, A	Sequence 99366, A	13	65.0	1245	5	US-10-027-632-207357	Sequence 207357,
C 399	13	65.0	692	6	US-10-027-632-99366 Sequence 99366, A	Sequence 99366, A	13	65.0	1245	5	US-10-027-632-207357	Sequence 207357,
C 400	13	65.0	694	6	US-10-149-759-67 Sequence 67, Appl	Sequence 67, Appl	13	65.0	1254	7	US-10-437-963-19139	Sequence 19139, A
C 401	13	65.0	713	4	US-09-925-065A-82461 Sequence 82461, A	Sequence 82461, A	13	65.0	1277	7	US-10-425-114-32433	Sequence 32433, A
C 402	13	65.0	714	7	US-10-767-701-9488 Sequence 9488, Ap	Sequence 9488, Ap	13	65.0	1281	9	US-10-617-320-1849	Sequence 1849, Ap
C 403	13	65.0	717	10	US-11-097-143-24035 Sequence 24035, A	Sequence 24035, A	13	65.0	1285	6	US-10-425-115-117753	Sequence 117753,
C 404	13	65.0	725	4	US-09-925-065A-80813 Sequence 80813, A	Sequence 80813, A	13	65.0	1288	6	US-10-017-161-2017	Sequence 2017, Ap
C 405	13	65.0	725	4	US-09-925-065A-80814 Sequence 80814, A	Sequence 80814, A	13	65.0	1288	6	US-10-292-798-1663	Sequence 1663, Ap
C 406	13	65.0	736	4	US-09-925-065A-932077 Sequence 932077, A	Sequence 932077, A	13	65.0	1310	8	US-10-425-115-160183	Sequence 160183,
C 407	13	65.0	741	6	US-10-369-493-33020 Sequence 33020, A	Sequence 33020, A	13	65.0	1316	9	US-10-450-763-5185	Sequence 5185, Ap
C 408	13	65.0	741	6	US-10-369-493-33172 Sequence 33172, A	Sequence 33172, A	13	65.0	1343	6	US-10-012-697-1340	Sequence 1340, A
C 409	13	65.0	750	6	US-10-369-493-41196 Sequence 41196, A	Sequence 41196, A	13	65.0	1343	9	US-10-779-543-23340	Sequence 23340, A
C 410	13	65.0	752	4	US-09-925-065A-84226 Sequence 84226, A	Sequence 84226, A	13	65.0	1348	6	US-10-120-988-404	Sequence 404, App
C 411	13	65.0	752	6	US-10-012-697-651 Sequence 651, App	Sequence 651, App	13	65.0	1380	6	US-10-369-493-44726	Sequence 44726, A
C 412	13	65.0	752	9	US-10-779-543-22651 Sequence 22651, A	Sequence 22651, A	13	65.0	1386	7	US-10-282-122A-34123	Sequence 34123, A
C 413	13	65.0	771	7	US-10-767-701-14188 Sequence 14188, A	Sequence 14188, A	13	65.0	1418	4	US-09-925-065A-58680	Sequence 58680, A
C 414	13	65.0	772	5	US-10-027-632-29156 Sequence 29156, A	Sequence 29156, A	13	65.0	1454	6	US-10-369-493-25184	Sequence 25184, A
C 415	13	65.0	772	6	US-10-027-632-29156 Sequence 29156, A	Sequence 29156, A	13	65.0	1475	7	US-10-371-472-30	Sequence 30, Appl
C 416	13	65.0	788	4	US-09-925-065A-69475 Sequence 69475, A	Sequence 69475, A	13	65.0	1475	7	US-10-371-472-30	Sequence 30, Appl
C 417	13	65.0	788	4	US-09-925-065A-69476 Sequence 69476, A	Sequence 69476, A	13	65.0	1475	7	US-10-371-472-30	Sequence 30, Appl
C 418	13	65.0	806	5	US-10-027-632-29717 Sequence 29717, A	Sequence 29717, A	13	65.0	1491	9	US-10-450-763-9000	Sequence 9000, Ap
C 419	13	65.0	806	6	US-10-027-632-29717 Sequence 29717, A	Sequence 29717, A	13	65.0	1502	7	US-10-072-012-23	Sequence 23, Appl
C 420	13	65.0	807	8	US-10-425-115-149036 Sequence 149036, A	Sequence 149036, A	13	65.0	1548	8	US-10-739-930-1177	Sequence 1177, Ap
C 421	13	65.0	810	4	US-09-925-065A-86355 Sequence 86355, A	Sequence 86355, A	13	65.0	1584	6	US-10-369-493-25422	Sequence 25422, A
C 422	13	65.0	830	7	US-10-435-114-5036 Sequence 5036, Ap	Sequence 5036, Ap	13	65.0	1596	7	US-10-260-238-3314	Sequence 3314, Ap
C 423	13	65.0	856	9	US-10-439-353A-96 Sequence 96, Appl	Sequence 96, Appl	13	65.0	1625	8	US-10-866-527-17	Sequence 17, Appl
C 424	13	65.0	857	6	US-10-012-697-715 Sequence 715, App	Sequence 715, App	13	65.0	1626	8	US-10-866-527-17	Sequence 17, Appl
C 425	13	65.0	857	9	US-10-779-543-22715 Sequence 22715, A	Sequence 22715, A	13	65.0	1641	7	US-10-425-114-28591	Sequence 28591, A
C 426	13	65.0	876	4	US-09-925-065A-715791 Sequence 715791, A	Sequence 715791, A	13	65.0	1657	8	US-10-425-115-170674	Sequence 170674,
C 427	13	65.0	876	4	US-09-925-065A-715792 Sequence 715792, A	Sequence 715792, A	13	65.0	1744	7	US-10-424-599-121358	Sequence 121358,
C 428	13	65.0	876	4	US-09-925-065A-715793 Sequence 715793, A	Sequence 715793, A	13	65.0	1803	3	US-09-815-242-4583	Sequence 4583, Ap
C 429	13	65.0	890	7	US-10-425-114-31415 Sequence 31415, A	Sequence 31415, A	13	65.0	1806	7	US-10-282-122A-7863	Sequence 7863, Ap
C 430	13	65.0	903	8	US-10-425-115-13115 Sequence 13115, A	Sequence 13115, A	13	65.0	1806	8	US-10-857-625-159	Sequence 31664, A
C 431	13	65.0	904	3	US-09-452-599-162 Sequence 162, App	Sequence 162, App	13	65.0	1806	8	US-10-857-625-159	Sequence 159, App
C 432	13	65.0	918	6	US-10-121-120-162 Sequence 121-120-162	Sequence 121-120-162	13	65.0	1824	3	US-10-259-194A-181	Sequence 512, App
C 433	13	65.0	918	6	US-10-121-120-162 Sequence 121-120-162	Sequence 121-120-162	13	65.0	1824	3	US-09-815-242-8270	Sequence 181, App
C 434	13	65.0	918	6	US-10-121-120-162 Sequence 121-120-162	Sequence 121-120-162	13	65.0	1824	3	US-09-815-242-8270	Sequence 8270, Ap
C 435	13	65.0	945	8	US-10-425-115-110999 Sequence 110999, A	Sequence 110999, A	13	65.0	1836	7	US-10-282-122A-8759	Sequence 8759, Ap
C 436	13	65.0	945	8	US-10-774-355A-753 Sequence 753, App	Sequence 753, App	13	65.0	1856	4	US-09-525-065A-707588	Sequence 707588,
C 437	13	65.0	963	6	US-10-424-599-47042 Sequence 47042, A	Sequence 47042, A	13	65.0	1902	7	US-10-437-963-64766	Sequence 64766, A
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C 439	13	65.0	1007	8	US-10-739-930-138 Sequence 351, App	Sequence 351, App	13	65.0	1935	3	US-09-771-161A-31	Sequence 31, Appl
C 440	13	65.0	1014	7	US-10-389-647-351 Sequence 126576, A	Sequence 126576, A	13	65.0	1997	8	US-10-425-115-10856	Sequence 10856, A
C 441	13	65.0	1015	8	US-10-425-115-126576 Sequence 34263, A	Sequence 34263, A	13	65.0	2000	3	US-09-938-842A-4728	Sequence 4728, Ap
C 442	13	65.0	1036	7	US-10-425-114-34263 Sequence 323709, A	Sequence 323709, A	13	65.0	2000	3	US-09-938-842A-4728	Sequence 4728, Ap
C 443	13	65.0	1039	5	US-10-027-632-323709 Sequence 323709, A	Sequence 323709, A	13	65.0	2000	3	US-10-424-599-38425	Sequence 38425, A
C 444	13	65.0	1039	5	US-10-027-632-323726 Sequence 323726, A	Sequence 323726, A	13	65.0	2003	10	US-11-097-143-23570	Sequence 23570, A
C 445	13	65.0	1039	5	US-10-027-632-323832 Sequence 323832, A	Sequence 323832, A	13	65.0	2009	4	US-09-925-065A-82092	Sequence 82092, A
C 446	13	65.0	1039	5	US-10-027-632-323909 Sequence 323909, A	Sequence 323909, A	13	65.0	2009	4	US-09-925-065A-82093	Sequence 82093, A
C 447	13	65.0	1039	6	US-10-027-632-323909 Sequence 323909, A	Sequence 323909, A	13	65.0	2009	4	US-09-925-065A-82094	Sequence 82094, A
C 448	13	65.0	1039	6	US-10-027-632-323909 Sequence 323909, A	Sequence 323909, A	13	65.0	2031	7	US-10-398-221-664	Sequence 664, App
C 449	13	65.0	1039	6	US-10-027-632-323926 Sequence 323926, A	Sequence 323926, A	13	65.0	2083	4	US-09-925-065A-547048	Sequence 547048,
C 450	13	65.0	1039	6	US-10-027-632-323926 Sequence 323926, A	Sequence 323926, A	13	65.0	2083	4	US-10-027-632-258567	Sequence 258567,
C 451	13	65.0	1041	7	US-10-437-963-80259 Sequence 80259, A	Sequence 80259, A	13	65.0	2083	6	US-10-027-632-258567	Sequence 258567,
C 452	13	65.0	1063	6	US-10-085-198-179 Sequence 179, App	Sequence 179, App	13	65.0	2089	3	US-09-764-864-1598	Sequence 1598, Ap
C 453	13	65.0	1092	3	US-09-778-844-90 Sequence 90, Appl	Sequence 90, Appl	13	65.0	2094	8	US-10-425-115-149035	Sequence 149035,
C 454	13	65.0	1092	5	US-10-021-657-5 Sequence 5, Appl1	Sequence 5, Appl1	13	65.0	2099	8	US-10-425-115-87145	Sequence 87145, A
C 455	13	65.0	1092	6	US-10-412-000-5 Sequence 5, Appl1	Sequence 5, Appl1	13	65.0	2100	8	US-10-425-115-10745	Sequence 10745, A
C 456	13	65.0	1118	4	US-09-925-065A-71947 Sequence 71947, A	Sequence 71947, A	13	65.0	2178	8	US-10-739-930-2282	Sequence 2282, Ap
C 457	13	65.0	1118	4	US-09-925-065A-71948 Sequence 71948, A	Sequence 71948, A	13	65.0	2311	3	US-09-800-729-66	Sequence 66, Appl
C 458	13	65.0	1129	8	US-10-343-903-31 Sequence 31, Appl	Sequence 31, Appl	13	65.0	2311	9	US-10-510-871-95	Sequence 95, Appl
C 459	13	65.0	1140	7	US-10-282-122A-34179 Sequence 34179, A	Sequence 34179, A	13	65.0	2354	9	US-10-450-763-4409	Sequence 4409, Ap
C 460	13	65.0	1155	3	US-09-815-242-8546 Sequence 8546, Ap	Sequence 8546, Ap	13	65.0	2357	10	US-11-097-143-35107	Sequence 35107, A
C 461	13	65.0	1155	3	US-09-815-242-8785 Sequence 8785, Ap	Sequence 8785, Ap	13	65.0	2388	3	US-09-933-767-154	Sequence 154, App
									2388	5	US-10-004-860-154	Sequence 154, App

535	13	65.0	2388	5	US-10-023-282-154	Sequence 154, App	c 608	13	65.0	7239	5	US-10-084-817-195	Sequence 195, App
c 536	13	65.0	2394	3	US-09-800-729-33	Sequence 33, Appl	c 609	13	65.0	7555	10	US-11-097-143-12403	Sequence 12403, A
c 537	13	65.0	2465	10	US-11-097-143-6122	Sequence 6122, Ap	c 610	13	65.0	7911	10	US-11-097-143-6790	Sequence 6790, Ap
538	13	65.0	2538	8	US-10-425-115-67067	Sequence 67067, A	611	13	65.0	8094	10	US-11-097-143-2992	Sequence 2992, Ap
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c 540	13	65.0	2631	3	US-09-801-368-43	Sequence 43, Appl	613	13	65.0	10200	10	US-11-097-143-19174	Sequence 19174, A
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c 543	13	65.0	2661	6	US-10-027-633-263854	Sequence 263854, A	c 616	13	65.0	12138	10	US-11-097-143-20566	Sequence 20566, A
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547	13	65.0	2905	4	US-09-925-065A-712237	Sequence 712237, App	620	13	65.0	15396	10	US-11-097-143-9031	Sequence 9031, Ap
548	13	65.0	2905	4	US-09-925-065A-712238	Sequence 712238, App	621	13	65.0	20099	5	US-10-177-744A-12	Sequence 12, Appl
549	13	65.0	2905	4	US-09-925-065A-712239	Sequence 712239, App	622	13	65.0	21407	10	US-11-097-143-40579	Sequence 40579, A
550	13	65.0	2905	4	US-09-925-065A-712240	Sequence 712240, App	623	13	65.0	21732	3	US-09-764-872-717	Sequence 717, App
c 551	13	65.0	2930	7	US-10-437-963-26536	Sequence 26536, A	624	13	65.0	30306	5	US-10-087-192-523	Sequence 523, App
552	13	65.0	3024	4	US-09-925-065A-711172	Sequence 711172, A	625	13	65.0	32503	10	US-11-097-143-16687	Sequence 16687, A
553	13	65.0	3024	4	US-09-925-065A-711173	Sequence 711173, A	626	13	65.0	35042	9	US-10-915-740A-2	Sequence 2, Appli
554	13	65.0	3309	10	US-11-097-143-6791	Sequence 6791, Ap	627	13	65.0	35962	8	US-10-775-169-234	Sequence 234, App
c 555	13	65.0	3366	3	US-09-925-301-246	Sequence 246, App	628	13	65.0	35962	8	US-10-473-126-2	Sequence 2, Appli
c 556	13	65.0	3430	7	US-10-437-963-101945	Sequence 101945, A	c 629	13	65.0	44325	3	US-09-997-722-226	Sequence 226, App
557	13	65.0	3477	7	US-10-437-963-75383	Sequence 75383, A	630	13	65.0	45588	9	US-10-893-315-180	Sequence 180, App
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562	13	65.0	3665	3	US-09-925-300-756	Sequence 756, App	635	13	65.0	61197	5	US-10-087-192-1924	Sequence 1924, Ap
c 563	13	65.0	3697	10	US-11-097-143-10675	Sequence 10675, A	636	13	65.0	61588	5	US-10-087-192-1570	Sequence 1570, Ap
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565	13	65.0	3897	6	US-10-412-000-7	Sequence 7, Appli	638	13	65.0	70419	6	US-10-004-113-40	Sequence 40, Appl
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567	13	65.0	4025	7	US-10-001-885-77	Sequence 77, Appl	640	13	65.0	75976	7	US-10-322-281-1942	Sequence 124, App
568	13	65.0	4025	10	US-11-057-447-77	Sequence 77, Appl	641	13	65.0	78313	7	US-10-052-482-124	Sequence 4, Appli
c 569	13	65.0	4026	5	US-10-171-587-17	Sequence 115, App	642	13	65.0	80246	3	US-09-728-552-4	Sequence 3, Appli
c 570	13	65.0	4026	5	US-10-981-277-17	Sequence 17, Appl	c 643	13	65.0	80595	3	US-09-728-552-3	Sequence 3, Appli
571	13	65.0	4169	9	US-10-915-740A-63	Sequence 63, Appl	c 644	13	65.0	84539	3	US-09-962-436-36	Sequence 36, Appl
c 572	13	65.0	4190	9	US-10-287-436A-186	Sequence 186, App	645	13	65.0	90442	5	US-10-843-641A-2495	Sequence 1, Appli
c 573	13	65.0	4190	9	US-10-287-436A-798	Sequence 798, App	646	13	65.0	90442	5	US-10-105-637-1	Sequence 43, Appl
c 574	13	65.0	4195	6	US-10-168-659-32	Sequence 32, Appl	647	13	65.0	90442	5	US-10-034-650-43	Sequence 3, Appli
c 575	13	65.0	4238	5	US-10-098-841-69	Sequence 69, Appl	648	13	65.0	92638	7	US-10-450-826-3	Sequence 52, Appl
576	13	65.0	4254	10	US-11-073-550-16	Sequence 16, Appl	649	13	65.0	94529	6	US-10-034-650-52	Sequence 37, Appl
577	13	65.0	4254	10	US-11-073-550-16	Sequence 16, Appl	c 650	13	65.0	99629	6	US-10-672-787-37	Sequence 39, Appl
c 578	13	65.0	4268	5	US-10-098-841-68	Sequence 68, Appl	651	13	65.0	100848	9	US-10-981-277-54	Sequence 54, Appl
579	13	65.0	4354	7	US-10-437-963-75382	Sequence 75382, A	c 652	13	65.0	103391	9	US-10-322-281-800	Sequence 114, App
c 580	13	65.0	4411	10	US-11-097-143-92335	Sequence 92335, Ap	c 653	13	65.0	133462	7	US-10-367-094-114	Sequence 69, Appl
c 581	13	65.0	4515	10	US-11-097-143-37387	Sequence 37387, A	654	13	65.0	140040	7	US-10-275-762-69	Sequence 2208, Ap
582	13	65.0	4590	7	US-10-282-122A-31991	Sequence 31991, A	c 655	13	65.0	143601	3	US-09-855-824-3	Sequence 1, Appli
583	13	65.0	4616	7	US-10-398-221-3730	Sequence 3730, Ap	c 656	13	65.0	161671	6	US-10-017-117-1	Sequence 26, Appl
584	13	65.0	4826	2	US-08-781-986A-275	Sequence 275, App	c 657	13	65.0	172825	9	US-10-981-277-26	Sequence 1438, Ap
585	13	65.0	4826	7	US-10-329-624-275	Sequence 275, App	c 658	13	65.0	177587	5	US-10-087-192-1438	Sequence 27, Appl
c 586	13	65.0	4981	7	US-10-437-963-26537	Sequence 26537, A	c 659	13	65.0	182508	9	US-10-981-277-27	Sequence 125, App
c 587	13	65.0	5019	10	US-11-097-143-16408	Sequence 16408, A	c 660	13	65.0	188053	8	US-10-417-375-125	Sequence 800, App
c 588	13	65.0	5356	6	US-10-269-909-40	Sequence 40, Appl	661	13	65.0	191584	7	US-10-322-281-126	Sequence 1126, Ap
c 589	13	65.0	5356	9	US-10-756-149-4427	Sequence 4427, App	c 662	13	65.0	212336	5	US-10-087-192-1126	Sequence 10, Appl
c 590	13	65.0	5358	6	US-10-264-049-944	Sequence 944, App	c 663	13	65.0	218802	9	US-10-897-508-1	Sequence 1, Appli
c 591	13	65.0	5621	10	US-11-097-143-40273	Sequence 40273, A	c 664	13	65.0	227246	5	US-10-322-281-314	Sequence 314, App
c 592	13	65.0	5813	9	US-10-956-157-4849	Sequence 4849, Ap	c 665	13	65.0	233060	5	US-10-087-192-97	Sequence 97, Appl
c 593	13	65.0	5817	8	US-10-723-860-1736	Sequence 1736, Ap	666	13	65.0	233060	5	US-10-087-192-97	Sequence 544, App
594	13	65.0	5853	8	US-10-723-860-6112	Sequence 6112, Ap	667	13	65.0	314364	9	US-10-917-647-3	Sequence 3, Appli
595	13	65.0	5972	10	US-11-097-143-6121	Sequence 6121, Ap	668	13	65.0	334462	9	US-10-496-011-1	Sequence 1, Appli
c 596	13	65.0	6069	6	US-10-085-198-27	Sequence 27, Appl	c 669	13	65.0	358246	6	US-10-322-696-76	Sequence 76, Appl
c 597	13	65.0	6157	6	US-10-085-198-29	Sequence 29, Appl	670	13	65.0	380963	9	US-10-737-082-5	Sequence 5, Appli
c 598	13	65.0	6195	6	US-10-085-198-25	Sequence 25, App	c 671	13	65.0	380963	9	US-10-765-790-5	Sequence 5, Appli
599	13	65.0	6254	3	US-09-860-670-279	Sequence 279, App	c 672	13	65.0	389432	9	US-10-737-082-34	Sequence 34, Appl
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c 603	13	65.0	6360	6	US-10-223-538-9	Sequence 538, A	676	13	65.0	389432	9	US-10-765-790-34	Sequence 34, Appl
c 604	13	65.0	6835	10	US-11-097-143-9322	Sequence 9322, Ap	c 677	13	65.0	389432	9	US-10-765-790-34	Sequence 34, Appl
c 605	13	65.0	7018	6	US-10-062-674-1565	Sequence 1565, Ap	678	13	65.0	389432	9	US-10-765-790-34	Sequence 34, Appl
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607	13	65.0	7159	7	US-10-329-624-302	Sequence 302, App	680	13	65.0	389432	9	US-10-765-790-34	Sequence 34, Appl

c 681	13	65.0	546025	8	US-10-719-993-6862	Sequence 6862, Ap	c 754	12	60.0	163	7	US-10-282-122A-1617	Sequence 1617, Ap
c 682	13	65.0	684707	7	US-10-398-221-9	Sequence 9, Appli	c 755	12	60.0	184	8	US-10-425-115-165038	Sequence 165038,
c 683	13	65.0	721377	9	US-10-461-862-163	Sequence 163, App	c 756	12	60.0	189	7	US-10-437-963-75501	Sequence 75501, A
c 684	13	65.0	822900	6	US-10-292-798-1393	Sequence 1393, Ap	c 757	12	60.0	193	7	US-10-242-535A-47068	Sequence 47068, A
c 685	13	65.0	1691139	5	US-10-067-514-1	Sequence 1, Appli	c 758	12	60.0	193	7	US-10-282-122A-2707	Sequence 2707, Ap
c 686	13	65.0	1691139	7	US-10-419-723-1	Sequence 1, Appli	c 759	12	60.0	193	7	US-10-085-783A-47068	Sequence 47068, A
c 687	13	65.0	1691139	9	US-10-255-120-1	Sequence 1, Appli	c 760	12	60.0	196	7	US-10-424-599-33593	Sequence 33593, A
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c 689	13	65.0	2242716	9	US-10-915-740A-1068	Sequence 1068, Ap	c 762	12	60.0	201	7	US-10-741-601-22371	Sequence 22371, A
c 690	13	65.0	2731748	7	US-10-297-465A-1	Sequence 1, Appli	c 763	12	60.0	201	8	US-10-719-993-13159	Sequence 13159, A
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c 694	12	60.0	20	7	US-10-688-706-190	Sequence 190, App	c 767	12	60.0	201	8	US-10-719-993-24786	Sequence 24786, A
c 695	12	60.0	229	7	US-10-688-706-229	Sequence 229, App	c 768	12	60.0	201	8	US-10-719-993-44456	Sequence 44456, A
c 696	12	60.0	24	5	US-10-021-758-9	Sequence 9, Appli	c 769	12	60.0	201	8	US-10-741-600-34651	Sequence 34651, A
c 697	12	60.0	25	5	US-10-098-263B-83338	Sequence 83338, A	c 770	12	60.0	201	8	US-10-741-600-34726	Sequence 34726, A
c 698	12	60.0	25	7	US-10-719-956-1044	Sequence 1044, Ap	c 771	12	60.0	201	8	US-10-741-600-42802	Sequence 42802, A
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c 700	12	60.0	25	7	US-10-719-956-150891	Sequence 150891,	c 773	12	60.0	201	8	US-10-741-600-54497	Sequence 54497, A
c 701	12	60.0	25	7	US-10-719-956-172010	Sequence 172010,	c 774	12	60.0	201	8	US-10-741-600-62617	Sequence 62617, A
c 702	12	60.0	25	7	US-10-719-956-182168	Sequence 182168,	c 775	12	60.0	209	5	US-10-027-632-54865	Sequence 54865, A
c 703	12	60.0	25	7	US-10-719-956-247146	Sequence 247146,	c 776	12	60.0	209	6	US-10-027-632-54865	Sequence 54865, A
c 704	12	60.0	25	7	US-10-719-956-247147	Sequence 247147,	c 777	12	60.0	211	8	US-10-425-115-161950	Sequence 161950,
c 705	12	60.0	25	7	US-10-719-956-519506	Sequence 519506,	c 778	12	60.0	212	3	US-09-764-860-74	Sequence 74, Appl
c 706	12	60.0	25	7	US-10-719-956-546709	Sequence 546709,	c 779	12	60.0	212	5	US-10-074-095-74	Sequence 74, Appl
c 707	12	60.0	25	7	US-10-719-956-589609	Sequence 589609,	c 780	12	60.0	212	6	US-10-212-872-74	Sequence 74, Appl
c 708	12	60.0	25	7	US-10-719-956-618632	Sequence 618632,	c 781	12	60.0	214	3	US-09-764-860-737	Sequence 737, App
c 709	12	60.0	25	7	US-10-719-956-657240	Sequence 657240,	c 782	12	60.0	214	3	US-09-764-860-738	Sequence 738, App
c 710	12	60.0	25	8	US-10-719-900-133201	Sequence 133201,	c 783	12	60.0	214	5	US-10-074-095-737	Sequence 737, App
c 711	12	60.0	25	8	US-10-719-900-133202	Sequence 133202,	c 784	12	60.0	214	5	US-10-074-095-738	Sequence 738, App
c 712	12	60.0	25	8	US-10-719-900-290057	Sequence 290057,	c 785	12	60.0	214	6	US-10-212-872-737	Sequence 737, App
c 713	12	60.0	25	8	US-10-719-900-178465	Sequence 178465,	c 786	12	60.0	214	6	US-10-212-872-738	Sequence 738, App
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## ALIGNMENTS

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; APPLICANT: Bhanot, Sanjay  
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; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-671-074-172

Query Match 100.0%; Score 20; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAACACAT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 GCTTTGGTTGGGCAACACAT 20

RESULT 2  
US-10-719-900-85415/c  
; Sequence 85415, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 85415  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-85415

Query Match 100.0%; Score 20; DB 8; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAACACAT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 21 GCTTTGGTTGGGCAACACAT 2

RESULT 3  
US-09-794-928A-12/c  
; Sequence 12, Application US/09794928A  
; Patent No. US20020127555A1  
; GENERAL INFORMATION:  
; APPLICANT: Baban, Soheyl  
; APPLICANT: Bernard, Monique  
; APPLICANT: Cherry, Elana  
; APPLICANT: Gosselin, Diane  
; APPLICANT: Hugo, Patrice  
; APPLICANT: Malette, Brigitte  
; APPLICANT: Miron, Pierre  
; APPLICANT: Prive, Charles  
; APPLICANT: Shazand, Kamran  
; TITLE OF INVENTION: ENDOMETRIOSIS-RELATED MARKERS AND USES THEREOF  
; FILE REFERENCE: 5600.71  
; CURRENT APPLICATION NUMBER: US/09/794,928A  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/225,745  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: US 60/185,063  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 254  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-794-928A-12

Query Match 100.0%; Score 20; DB 3; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAACACAT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 90 GCTTTGGTTGGGCAACACAT 71

RESULT 4  
US-10-242-535A-24143/c  
; Sequence 24143, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; CURRENT FILING DATE: 2002-09-12



; PRIOR APPLICATION NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24143  
; LENGTH: 303  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2)..(2)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (6)..(6)  
; OTHER INFORMATION: n is a, c, g, or t  
; NAME/KEY: misc\_feature  
; LOCATION: (196)..(196)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (236)..(236)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (238)..(238)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (266)..(266)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (274)..(274)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-242-535A-24143

Query Match 100.0%; Score 20; DB 7; Length 303;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20  
||| ||||| ||||| ||||| |||||  
Db 184 GCTTTGGTTGGCAACACAT 165

RESULT 5  
US-10-085-783A-24143/c  
; Sequence 24143, Application US/10085783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US/10/085,783A  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24143

; LENGTH: 303  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2)..(2)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (6)..(6)  
; OTHER INFORMATION: n is a, c, g, or t  
; NAME/KEY: misc\_feature  
; LOCATION: (196)..(196)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (236)..(236)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (238)..(238)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (266)..(266)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (274)..(274)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-085-783A-24143

Query Match 100.0%; Score 20; DB 7; Length 303;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20  
||| ||||| ||||| ||||| |||||  
Db 184 GCTTTGGTTGGCAACACAT 165

RESULT 6  
US-10-242-535A-35649/c  
; Sequence 35649, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 35649  
; LENGTH: 447  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (7)..(7)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-242-535A-35649



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Query Match      100.0%; Score 20; DB 7; Length 447;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20
    |||||
Db 95 GCTTTGGTTGGCAACACAT 76

RESULT 7
US-10-085-783A-35649/c
; Sequence 35649, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4331/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35649
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-35649

Query Match      100.0%; Score 20; DB 7; Length 447;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20
    |||||
Db 95 GCTTTGGTTGGCAACACAT 76

RESULT 8
US-10-505-680-708
; Sequence 708, Application US/10505680
; Publication No. US2005009592A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Jazaeri, Amir A.
; APPLICANT: Boyd, Jeff
; APPLICANT: Liu, Edison T.
; TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THERAPEUTIC TA
; FILE REFERENCE: 4239-64452
; CURRENT APPLICATION NUMBER: US/10/505,680
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/357,031
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 822
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 708
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(520)
; OTHER INFORMATION: "n" represents an unknown nucleotide
```

```
US-10-505-680-708

Query Match      100.0%; Score 20; DB 9; Length 520;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20
    |||||
Db 163 GCTTTGGTTGGCAACACAT 182

RESULT 9
US-10-450-763-20856/c
; Sequence 20856, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 20856
; LENGTH: 2514
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(2511)
; OTHER INFORMATION: 99% homologous to synthetic construct Pax3-forkhead fusion
; OTHER INFORMATION: protein, accession number AF178854, Smith-Waterman Score=4401.
US-10-450-763-20856

Query Match      100.0%; Score 20; DB 9; Length 2514;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20
    |||||
Db 2466 GCTTTGGTTGGCAACACAT 2447

RESULT 10
US-10-391-530-1/c
; Sequence 1, Application US/10391530
; Publication No. US20040110227A1
; GENERAL INFORMATION:
; APPLICANT: Levanon, Erez
; APPLICANT: Toporik, Amir
; APPLICANT: Akiva, Pini
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR IDENTIFYING PUTATIVE FUSION TRANSCRIPTS,
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREFROM AND POLYNUCLEOTIDE SEQUENCES RELAT
; FILE REFERENCE: 25835
; TITLE OF INVENTION: METHODS AND KITS UTILIZING SAME
; CURRENT APPLICATION NUMBER: US/10/391,530
; CURRENT FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-391-530-1

Query Match      100.0%; Score 20; DB 7; Length 2827;
Best Local Similarity 100.0%; Pred. No. 0.044;
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```
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTTGGTGGCAACACAT 20
Db 2647 GCTTTGGTGGCAACACAT 2628

RESULT 11
US-10-391-530-3/c
; Sequence 3, Application US/10391530
; Publication No. US20040110227A1
; GENERAL INFORMATION:
; APPLICANT: Levanon, Erez
; APPLICANT: Toporik, Amir
; APPLICANT: Akiva, Pini
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR IDENTIFYING PUTATIVE FUSION TRANSCRIPTS,
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREFROM AND POLYNUCLEOTIDE SEQUENCES RELA
; FILE REFERENCE: 25835
; CURRENT APPLICATION NUMBER: US/10/391,530
; CURRENT FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3200
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-391-530-3
Query Match 100.0%; Score 20; DB 7; Length 3200;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTTGGTGGCAACACAT 20
Db 2511 GCTTTGGTGGCAACACAT 2492

RESULT 12
US-10-391-530-2/c
; Sequence 2, Application US/10391530
; Publication No. US20040110227A1
; GENERAL INFORMATION:
; APPLICANT: Levanon, Erez
; APPLICANT: Toporik, Amir
; APPLICANT: Akiva, Pini
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR IDENTIFYING PUTATIVE FUSION TRANSCRIPTS,
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREFROM AND POLYNUCLEOTIDE SEQUENCES RELA
; FILE REFERENCE: 25835
; CURRENT APPLICATION NUMBER: US/10/391,530
; CURRENT FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-391-530-2
Query Match 100.0%; Score 20; DB 7; Length 3517;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTTGGTGGCAACACAT 20
Db 2022 GCTTTGGTGGCAACACAT 2003

RESULT 13
US-10-671-074-11/c
; Sequence 11, Application US/10671074
; Publication No. US20040097459A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Veniant-Ellison, Murielle
; APPLICANT: Lindberg, Richard A.
; APPLICANT: Shutter, John R.
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX OIA EXPRESSION
; FILE REFERENCE: AMGN0001-101
; CURRENT APPLICATION NUMBER: US/10/671,074
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 11
; LENGTH: 4945
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (429)...(2387)
US-10-671-074-11
Query Match 100.0%; Score 20; DB 7; Length 4945;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTTGGTGGCAACACAT 20
Db 2339 GCTTTGGTGGCAACACAT 2320

RESULT 14
US-10-007-926A-134/c
; Sequence 134, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; FILE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
; LENGTH: 5723
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: forkhead box oia (rhabdomyosarcoma) (FOXO1A)
; OTHER INFORMATION: gene.
US-10-007-926A-134
Query Match 100.0%; Score 20; DB 6; Length 5723;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTTGGTGGCAACACAT 20
Db 2305 GCTTTGGTGGCAACACAT 2286

RESULT 15
US-10-341-434-52/c
; Sequence 52, Application US/10341434
```

; Publication No. US20030215835A1  
; GENERAL INFORMATION:  
; APPLICANT: Origene Technologies  
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes  
; FILE REFERENCE: 9U 204 205 R1  
; CURRENT APPLICATION NUMBER: US/10/341,434  
; CURRENT FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: US 60/348,164  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: US 60/348,119  
; PRIOR FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 238  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52  
; LENGTH: 5723  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (386)..(2350)  
; OTHER INFORMATION:  
US-10-341-434-52

Query Match 100.0%; Score 20; DB 6; Length 5723;  
Best Local Similarity 100.0%; Pred. No. 0.045;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20  
|||||  
Db 2305 GCTTTGGTTGGCAACACAT 2286

RESULT 16  
US-10-671-074-4/c  
; Sequence 4, Application US/10671074  
; Publication No. US20040097459A1  
; GENERAL INFORMATION:  
; APPLICANT: Dobie, Kenneth W.  
; APPLICANT: Bhanot, Sanjay  
; APPLICANT: Veniant-Ellison, Murielle  
; APPLICANT: Lindberg, Richard A.  
; APPLICANT: Shutter, John R.  
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION  
; FILE REFERENCE: AMGN0001-101  
; CURRENT APPLICATION NUMBER: US/10/671,074  
; CURRENT FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: US 10/260,203  
; PRIOR FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 176  
; SEQ ID NO 4  
; LENGTH: 5723  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (386)...(2353)  
US-10-671-074-4

Query Match 100.0%; Score 20; DB 7; Length 5723;  
Best Local Similarity 100.0%; Pred. No. 0.045;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20  
|||||  
Db 2305 GCTTTGGTTGGCAACACAT 2286

RESULT 17  
US-10-956-157-760/c  
; Sequence 760, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 760  
; LENGTH: 5723  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-760

Query Match 100.0%; Score 20; DB 9; Length 5723;  
Best Local Similarity 100.0%; Pred. No. 0.045;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20  
|||||  
Db 2305 GCTTTGGTTGGCAACACAT 2286

RESULT 18  
US-10-450-763-20857/c  
; Sequence 20857, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 20857  
; LENGTH: 5833  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (157)..(585)  
; OTHER INFORMATION: 31% homologous to Homo sapiens fork head domain  
; OTHER INFORMATION: protein, accession number U02310, Smith-Waterman Score=53.  
US-10-450-763-20857

Query Match 100.0%; Score 20; DB 9; Length 5833;  
Best Local Similarity 100.0%; Pred. No. 0.045;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20  
|||||  
Db 2357 GCTTTGGTTGGCAACACAT 2338

RESULT 19  
US-10-671-074-40  
; Sequence 40, Application US/10671074  
; Publication No. US20040097459A1  
; GENERAL INFORMATION:  
; APPLICANT: Dobie, Kenneth W.  
; APPLICANT: Bhanot, Sanjay  
; APPLICANT: Veniant-Ellison, Murielle  
; APPLICANT: Lindberg, Richard A.  
; APPLICANT: Shutter, John R.  
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION

; FILE REFERENCE: AMGN0001-101  
; CURRENT APPLICATION NUMBER: US/10/671,074  
; CURRENT FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: US 10/260,203  
; PRIOR FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 176  
; SEQ ID NO 40  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-671-074-40

Query Match 95.0%; Score 19; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTTGGTTGGCAACACAT 20  
|||||  
DB 1 CTTTGGTTGGCAACACAT 19

RESULT 20  
US-10-671-074-118/c  
; Sequence 118, Application US/10671074  
; Publication No. US20040097459A1  
; GENERAL INFORMATION:  
; APPLICANT: Dobie, Kenneth W.  
; APPLICANT: Bhanot, Sanjay  
; APPLICANT: Veniant-Ellison, Murielle  
; APPLICANT: Lindberg, Richard A.  
; APPLICANT: Shutter, John R.  
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION  
; FILE REFERENCE: AMGN0001-101  
; CURRENT APPLICATION NUMBER: US/10/671,074  
; CURRENT FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: US 10/260,203  
; PRIOR FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 176  
; SEQ ID NO 118  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-671-074-118

Query Match 95.0%; Score 19; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTTGGTTGGCAACACAT 20  
|||||  
DB 20 CTTTGGTTGGCAACACAT 2

RESULT 21  
US-09-938-842A-4239/c  
; Sequence 4239, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SCRIP1300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647

; FILE REFERENCE: AMGN0001-101  
; CURRENT APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 4239  
; LENGTH: 2000  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-4239

Query Match 85.0%; Score 17; DB 3; Length 2000;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAACA 17  
|||||  
DB 327 GCTTTGGTTGGCAACA 311

RESULT 22  
US-09-938-842A-4239/c  
; Sequence 4239, Application US/09938842A  
; Publication No. US2004009476A9  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SCRIP1300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 4239  
; LENGTH: 2000  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-4239

Query Match 85.0%; Score 17; DB 3; Length 2000;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAACA 17  
|||||  
DB 327 GCTTTGGTTGGCAACA 311

RESULT 23  
US-10-671-074-41  
; Sequence 41, Application US/10671074  
; Publication No. US20040097459A1  
; GENERAL INFORMATION:  
; APPLICANT: Dobie, Kenneth W.  
; APPLICANT: Bhanot, Sanjay  
; APPLICANT: Veniant-Ellison, Murielle  
; APPLICANT: Lindberg, Richard A.  
; APPLICANT: Shutter, John R.  
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION  
; FILE REFERENCE: AMGN0001-101  
; CURRENT APPLICATION NUMBER: US/10/671,074  
; CURRENT FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: US 10/260,203  
; PRIOR FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 176  
; SEQ ID NO 41



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; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 107214
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(405)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_6782C.1
US-10-424-599-107214

Query Match          75.0%; Score 15; DB 7; Length 405;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGTGGGCAACACAT 20
        |||
Db       277 GGTGGGCAACACAT 263

RESULT 29
US-10-430-201-4459
; Sequence 4459, Application US/10430201
; Publication No. US20040162679A1
; GENERAL INFORMATION:
; APPLICANT: Li, Linheng
; TITLE OF INVENTION: Method for Predicting Gene Potential and Cell Commitment
; FILE REFERENCE: 40716 (IP-010)
; CURRENT APPLICATION NUMBER: US/10/430,201
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/370,114
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 4879
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4459
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (180)..(180)
; OTHER INFORMATION: n is a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (185)..(185)
; OTHER INFORMATION: n is a, c, g, or t
US-10-430-201-4459

Query Match          75.0%; Score 15; DB 7; Length 406;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGTGGGCAACACAT 20
        |||
Db       267 GGTGGGCAACACAT 281

RESULT 30
US-10-430-201-4460
; Sequence 4460, Application US/10430201
; Publication No. US20040162679A1
; GENERAL INFORMATION:
; APPLICANT: Li, Linheng
; TITLE OF INVENTION: Method for Predicting Gene Potential and Cell Commitment
```

```
; FILE REFERENCE: 40716 (IP-010)
; CURRENT APPLICATION NUMBER: US/10/430,201
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/370,114
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 4879
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4460
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (180)..(180)
; OTHER INFORMATION: n is a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (185)..(185)
; OTHER INFORMATION: n is a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (226)..(226)
; OTHER INFORMATION: n is a, c, g, or t
US-10-430-201-4460

Query Match          75.0%; Score 15; DB 7; Length 406;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGTGGGCAACACAT 20
        |||
Db       267 GGTGGGCAACACAT 281

RESULT 31
US-09-918-995-32485/C
; Sequence 32485, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32485
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(498)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32485

Query Match          75.0%; Score 15; DB 3; Length 498;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTTGGTTGGGCAA 15
        |||
Db       253 GCTTTGGTTGGGCAA 239

RESULT 32
US-09-764-872-161
; Sequence 161, Application US/09764872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
```





; PRIOR FILING DATE: 1996-11-22  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 66  
; LENGTH: 1342  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1238)..(1238)  
; OTHER INFORMATION: n equals a, t, g, or c  
US-09-956-004-66

Query Match 75.0%; Score 15; DB 3; Length 1342;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAA 15  
|||  
Db 614 GCTTTGGTTGGCAA 628

## RESULT 37

US-10-808-570-66  
; Sequence 66, Application US/10808570  
; Publication No. US20040192903A1  
; GENERAL INFORMATION:  
; APPLICANT: Patrick J. Dillon et al.  
; TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands  
; FILE REFERENCE: PB324D1  
; CURRENT APPLICATION NUMBER: US/10/808,570  
; CURRENT FILING DATE: 2004-03-25  
; PRIOR APPLICATION NUMBER: US/09/956,004  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 08/976,259  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/061,953  
; PRIOR FILING DATE: 1997-10-14  
; PRIOR APPLICATION NUMBER: 60/031,626  
; PRIOR FILING DATE: 1996-11-22  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 66  
; LENGTH: 1342  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1238)..(1238)  
; OTHER INFORMATION: n equals a, t, g, or c  
US-10-808-570-66

Query Match 75.0%; Score 15; DB 8; Length 1342;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAA 15  
|||  
Db 614 GCTTTGGTTGGCAA 628

## RESULT 38

US-10-108-260A-1546/c  
; Sequence 1546, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1546  
; LENGTH: 1550  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-1546

Query Match 75.0%; Score 15; DB 6; Length 1550;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAA 15  
|||  
Db 269 GCTTTGGTTGGCAA 255

## RESULT 39

US-10-282-122A-9084  
; Sequence 9084, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9084  
; LENGTH: 2154  
; TYPE: DNA  
; ORGANISM: Acinetobacter baumannii  
US-10-282-122A-9084

Query Match 75.0%; Score 15; DB 7; Length 2154;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAA 15  
|||  
Db 860 GCTTTGGTTGGCAA 874

RESULT 40  
US-10-094-749-916  
; Sequence 916, Application US/10094749  
; Publication No. US20030219741A1  
; GENERAL INFORMATION:  
; APPLICANT: ISOGAI, TAKAO  
; APPLICANT: SUGIYAMA, TOMOYASU  
; APPLICANT: OTSUKI, TETSUJI  
; APPLICANT: WAKAMATSU, AI  
; APPLICANT: SATO, HIROYUKI  
; APPLICANT: ISHII, SHIZUKO  
; APPLICANT: YAMAMOTO, JUN-ICHI  
; APPLICANT: ISONO, YUUKO  
; APPLICANT: HIO, YURI  
; APPLICANT: OTSUKA, KAORU  
; APPLICANT: NAGAI, KEIICHI  
; APPLICANT: IRIE, RYOTARO  
; APPLICANT: TAMECHIKA, ICHIRO  
; APPLICANT: SEKI, NAOHICO  
; APPLICANT: YOSHIKAWA, TSUTOMU  
; APPLICANT: OTSUKA, MOTOKYUKI  
; APPLICANT: NAGAHARI, KENJI  
; APPLICANT: MASUHO, YASUHIKO  
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA  
; FILE REFERENCE: 084335/0160  
; CURRENT APPLICATION NUMBER: US/10/094,749  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 60/350,435  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: JP 2001-328381  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 3381  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 916  
; LENGTH: 3059  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-094-749-916

Query Match 75.0%; Score 15; DB 6; Length 3059;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTGGGCAACACAT 20  
Db 1579 GGTGGGCAACACAT 1593

RESULT 41  
US-11-097-143-32554/c  
; Sequence 32554, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: DROSOPHILA GENES.  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 916  
; LENGTH: 3366  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-11-097-143-32554/c

; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32554  
; LENGTH: 3342  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-11-097-143-32554

Query Match 75.0%; Score 15; DB 10; Length 3342;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGCAAC 16  
Db 648 CTTTGGTTGGCAAC 634

RESULT 42  
US-11-097-143-23078/c  
; Sequence 23078, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: DROSOPHILA GENES.  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23078  
; LENGTH: 3366  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-11-097-143-23078

Query Match 75.0%; Score 15; DB 10; Length 3366;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGCAAC 16  
Db 3075 CTTTGGTTGGCAAC 3061

RESULT 43  
US-10-002-775-10  
; Sequence 10, Application US/10002775  
; Publication No. US20020102651A1  
; GENERAL INFORMATION:

; APPLICANT: Gordon Freeman  
; APPLICANT: Vassiliki Bousiotis  
; APPLICANT: Tatyana Chernova  
; APPLICANT: Nelly Malenkovich  
; TITLE OF INVENTION: NOVEL B7-4 MOLECULES AND USES THEREFOR  
; FILE REFERENCE: GNN-004ADV  
; CURRENT APPLICATION NUMBER: US/10/002,775  
; PRIOR FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: US 09/644,934  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: 60/150,390  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 3593  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (17)..(889)  
US-10-002-775-10

Query Match 75.0%; Score 15; DB 5; Length 3593;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGTGGGCAACACAT 20  
|||||  
DB 3406 GGTGGGCAACACAT 3420

RESULT 44  
US-10-115-615-22  
; Sequence 22, Application US/10115615  
; Publication No. US20030044768A1  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Clive  
; APPLICANT: Freeman, Gordon  
; APPLICANT: Chaudhary, Divya  
; TITLE OF INVENTION: PD-1, A RECEPTOR FOR B7-4, AND USES THEREFOR  
; FILE REFERENCE: GNN-004C  
; CURRENT APPLICATION NUMBER: US/10/115,615  
; CURRENT FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: US 60/281064  
; PRIOR FILING DATE: 2001-04-02  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 3593  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (17)..(889)  
US-10-115-615-22

Query Match 75.0%; Score 15; DB 5; Length 3593;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGTGGGCAACACAT 20  
|||||  
DB 3406 GGTGGGCAACACAT 3420

RESULT 45  
US-10-764-420-1546  
; Sequence 1546, Application US/10764420  
; Publication No. US20050084872A1  
; GENERAL INFORMATION:  
; APPLICANT: Lum, Pek Yee  
; APPLICANT: Tan, Yejun

; APPLICANT: Dai, Hongyue  
; TITLE OF INVENTION: Methods For Determining Whether An Agent  
; FILE REFERENCE: ROSA122057  
; CURRENT APPLICATION NUMBER: US/10/764,420  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: US 60/442,797  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: US 60/474,413  
; PRIOR FILING DATE: 2003-05-30  
; NUMBER OF SEQ ID NOS: 3683  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1546  
; LENGTH: 3593  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-764-420-1546

Query Match 75.0%; Score 15; DB 9; Length 3593;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGTGGGCAACACAT 20  
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DB 3406 GGTGGGCAACACAT 3420

RESULT 46  
US-10-631-467-1140  
; Sequence 1140, Application US/10631467  
; Publication No. US20050208496A1  
; GENERAL INFORMATION:  
; APPLICANT: Genox Research Inc.  
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive  
; FILE REFERENCE: 3462.1005-000  
; CURRENT APPLICATION NUMBER: US/10/631,467  
; CURRENT FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: JP 2003-077212  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: JP 2002-229312  
; PRIOR FILING DATE: 2002-08-06  
; NUMBER OF SEQ ID NOS: 2086  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1140  
; LENGTH: 3593  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-631-467-1140

Query Match 75.0%; Score 15; DB 9; Length 3593;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGTGGGCAACACAT 20  
|||||  
DB 3406 GGTGGGCAACACAT 3420

RESULT 47  
US-10-758-672A-18  
; Sequence 18, Application US/10758672A  
; Publication No. US20040185037A1  
; GENERAL INFORMATION:  
; APPLICANT: Han, et al.  
; TITLE OF INVENTION: HUMAN E3 ALPHA UBIQUITIN LIGASE FAMILY  
; FILE REFERENCE: 01017/35966B  
; CURRENT APPLICATION NUMBER: US/10/758,672A  
; CURRENT FILING DATE: 2004-01-15  
; PRIOR APPLICATION NUMBER: US 09/724,126  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 60/187,911  
; PRIOR FILING DATE: 2000-03-08

; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 5205  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (662)..(662)  
; OTHER INFORMATION: n = a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (668)..(668)  
; OTHER INFORMATION: n = a, c, g, or t  
US-10-758-672A-18

Query Match 75.0%; Score 15; DB 8; Length 5205;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTGGGCAACACAT 20  
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Db 1518 GGTGGGCAACACAT 1532

## RESULT 48

US-10-758-636A-18  
; Sequence 18, Application US/10758636A  
; Publication No. US20050089876A1  
; GENERAL INFORMATION:  
; APPLICANT: Han, et al.

; TITLE OF INVENTION: HUMAN E3 ALPHA UBIQUITIN LIGASE FAMILY  
; FILE REFERENCE: 01017/35966C  
; CURRENT APPLICATION NUMBER: US/10/758,636A  
; CURRENT FILING DATE: 2004-01-15  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 60/187,911  
; PRIOR FILING DATE: 2000-03-08  
; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 5205  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (662)..(662)  
; OTHER INFORMATION: n = a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (668)..(668)  
; OTHER INFORMATION: n = a, c, g, or t  
US-10-758-636A-18

Query Match 75.0%; Score 15; DB 9; Length 5205;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTGGGCAACACAT 20  
|||||  
Db 1518 GGTGGGCAACACAT 1532

## RESULT 49

US-10-357-819-9  
; Sequence 9, Application US/10357819  
; Publication No. US20040259774A1  
; GENERAL INFORMATION:  
; APPLICANT: Alvarez, Enrique  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gangolli, Esna A.  
; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Gorman, Linda  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Li, Li  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD;  
; FILE REFERENCE: 21402-538A

; CURRENT APPLICATION NUMBER: US/10/357,819  
; CURRENT FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: 09/520,781  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 09/584,411  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: 09/783,436  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 10/085,198  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/353,301  
; PRIOR FILING DATE: 2002-02-01  
; PRIOR APPLICATION NUMBER: 60/355,099  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: 60/356,424  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 60/358,239  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: 60/358,608  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/359,367  
; PRIOR FILING DATE: 2002-02-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 142

; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 9  
; LENGTH: 5466  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (66)..(5312)  
US-10-357-819-9

Query Match 75.0%; Score 15; DB 8; Length 5466;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTGGGCAACACAT 20  
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Db 1628 GGTGGGCAACACAT 1642

## RESULT 50

US-11-097-143-23077/c  
; Sequence 23077, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: DROSOPHILA GENES.  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832

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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23077
; LENGTH: 5492
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-23077

Query Match      75.0%; Score 15; DB 10; Length 5492;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTTTGGTTGGCAAC 16
Db      4201 CTTTGGTTGGCAAC 4187
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Search completed: May 7, 2006, 23:36:31  
Job time : 1085 secs

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